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8.9 168069	8.9 113880	8.9 85916	•	•	8.9 250793	8.9 250022	8.9 182870	8.9 146570		9.0 253151	-	9.0 250823	9.0 333321	9.0 148486	Ļ	<u>, , </u>	9.1 174574	9.1 8056	9.1 183648	N	9.2 185342	'n	9.3 181430	9.3 177444	9.3 273275
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## ALIGNMENTS

RESULT 1

REFERENCE 4 AUTHORS E TITLE C JOURNAL C	-		Cl JOURNAL UI REFERENCE 2 AUTHORS E	TILLE I	REFERENCE 1	VERSION P KEYWORDS H SOURCE P ORGANISM P	ACCESSION
Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA 4 (bases 1 to 84203) Ecker,J.R. Direct Submission Submitted (01-DEC-1998) Arabidopsis thaliana Genome Center, Submitted (01-DEC-1998) Wiversity of Pennsylvania, 38th Street and Department of Biology, University of Pennsylvania, 19104-6018, USA	9 E E E	Direct Submission Submitted (16-JUN-1998) Arabidopsis thaliana Genome Center, Bubmitted (16-JUN-1998) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA 3 (bases 1 to 84201)	chromosome I Unpublished 2 (bases 1 to 84203) Ecker,J.R.	Shinn, P., Altafi, H., Bei, O., Chin, C., Chiou, J., Cohoi, E., Conn, L., Conway, A., Gonzales, A., Hansen, M., Howing, B., Koo, T., Law, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, K., Liu, S., Mukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H., Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M., Yu, G., Federspiel, N.A., Theologis, A. and Ecker, J.R.  Genomic sequence for Arabidopsis thaliana BAC T25N20 from	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  1 (bases 1 to 84203)  Johnson-Hopson,C., Brooks,S., Buehler,E., Chao,Q., Khan,S., Kim,C.,	AC005106.2 GI:6587719 HTG. Arabidopsis thaliana (thale cress) Arabidopsis thaliana	AC005106 84203 bp DNA linear PLN 28-JUN-2000 Genomic sequence for Arabidopsis thaliana BAC T25N20 from Chromosome I, complete sequence. AC005106

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REFERENCE
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Direct Submission

Direct Submission

Submitted (28-JUN-2000) Arabidopsis thaliana Genome Center, Submitted
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Submitted (10-JUN-2000) Arabidopsis thaliana Genome Center,
Department of Biology, University of Pennsylvania, 38th Street
Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA
7 (bases 1 to 84203)
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Submitted (16-DEC-1999) Arabidopsis thaliana Genome Center
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                                                                                                                                                                                                                    Join(9304. .11268,11387. .11513,11607. .11
12698. .12784,13257. .13356,13451. .14263)
/note="unknown protein; similar to ESTs gb
gb[AI998699.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(1491. .2159,2389. .2452,2568. .2697, 3061. .3118,3369. .3457,4022. .4139,4246. .4353)) /note="similar to YUP8H12.1 gb|AAB71441.1; similar to gb|Ai996871.1"
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ssypsrvsslæfdtsslkstdkigscassrfaftvsrdgldtvkpmcltltdtsstk
lghntgayisplnarsfsfaspaarseffgfrrsffastmparttdrhsigtlrdd
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VSIVSTQIRRRHVSLSQRF"
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chromosome="1"
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KPKKEFNTKSKSTYPELVNPDVREERRGRRGGGTDKORLERE I KGMLTDAGWTIDYKP
RRNOSYLDAVYNPSGTAYWSI I KAYDALLKOLLDEGVDARPRKDTAAVASVSEEI VN
KLARRAKKTRSEMTKKWKQNSSGSDSENKSEGAYTDTSEER I RSJ KLJGGKSTKKGR
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NGFNPYSGKRTLLSWLI ESGVVQLRQKVOYMRRRGAKVMLEGWI TREGIHCDCCSKIL
TVSRPEIHAGSKSCOPEONI YLESGASLLQCOYMARWOKDATNLALHQVUTDGDDPN
DDAGGI (GDGGDLI (CDGCPSTYHQNCLGMOYL)PSGDMCPNCTCKFCDAAVASGGKD
GNFI SILLSCGMCERRYHQLCLNDEAHKVQS FGSASS FCGPKCLELFEKLQKYLGVKTE
IEGGY SWSLLHR VDTDSDTNSQMSAQRI ENNSKLAVGLAI MDECCTLEI VUDRRSGVDLI
RNVLYNCGSNPNR INYTGFYTAILERADE I SAASLRRHGMOLLEMPFIGTRHI YRRQ
GMCRRLFDAL ESAMRSLKVEKLIV I PAI PDFLHAWTGNFGFTPLDDSVRKEMRSLNTLV
GGGROLLFDAL ESAMRSLKVEKLIV I PAI PDFLHAWTGNFGFTPLDDSVRKEMRSLNTLN
AANCYKDILASDEDNILVSVETAMGTI CKPKDELSRHFRGEESGISSSCOQITLKSGT
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SCYNGPVTITAVGSLSKVPRDILEVVSSTGISLYHEVATTLMEISRPPLWIPPGFYSN
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VCRRICGPGIAGQGVDNFITHLSTREHELKRQRFTNPKGEPPLDSCPENATRGGNQS"
complement (join(17577. 18026, 18231. 18796, 18981. 19410)
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DLSSISQEVKSEQTSSNLDGVPSCKDYNILVPGAKLDKSKDDAFADGFLL"
Complement (join 114820...14957,15038...15420,15643...15721))
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SFMKMNKLDIFEFDEYDGFDSANLMRKRFDNGSVGVRGRSSFASRRVDSSVGRSGSGR
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                                                                                                                           ISLEHGGYSYIKCEAVVSEGHICGHVAHMNCALRAYLAGTIGGSMGLDTEYYCRRCDA
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FILVVDYSDSGARENDTLOSLQDVPTIGFIPFDHBAEMHKLEEEIGBVVLRALRKAQE
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                                                                                           TKLKEMEEVAKGFGRTPRGVLEEYFHLNIED"
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join(16415. .16661,16811.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="codon recognized: AAC; putative tRNA-Asn"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'product="tRNA-Asn"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .17133,17234. .17317)
EST emb | Z34709.1"
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**ERNA** 

CDS

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codon\_start=1

CDS

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RESULT 2
AC007153
                               LOCUS
DEFINITION
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Best Local S
Matches 699
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  AC007153
Arabidopsis thaliana complete sequence.
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                                                                                                                                                                                                                                   CATCAAAACATATTTGGCGTTATTATTTCTGTGGTCACTTGAATA 703
                                                                                                                                                                                                                                                                                                                                                       TTGCTCTCTCTCTTTTAAAATGGTAAACTGGTAAAGATAGGAGACTCAATTTCTAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                      CTTATTGGCTTGGCAAGATTCCATAAGTTTATTTCACCAAAAAGGAAAGGGTACTTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTATTGGCTTGGCAAGATTCCATAAGTTTATTTCACCAAAAAGGAAAGAGTACTTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TANATAAATATAGAAAGTGAACAAAAAAAAATTAGTGGAAAAGGTAACTGGAAAGGAAAAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAATTATTGTAGACGAGTGGTCCATATATAGATGGTGAAATGAAATGAATATTGAGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAAATTATTGTAGACGAGTGGTCCATATATAGATGGTGAAATGAAATGAAATGATTGAGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTTTTTAGTACTTGTTTTTCTTTTTTGGGTTCAACTAGTTACTTTTTTCCTTTGACATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTTTTTAGTACTTGTTTTTTTTTTTGGGTTCAACTAGTTACTTTTTTTCCTTTGACATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCCGCGTGTAATTAAGTTTTATGAAATGTGGTTATTTTGTAGGTCACGTGAAATTTATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCCGCGTGTAATTAAGTTTTATGAAATGTGGTTATTTTGTAGGTCACGTGAAATTTATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGACCATACCGGTTAATAATATTCTAACCGGTTTATAAGTTTACATAAATCATTTACTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCCTGTCTTTAAACCTCGTAAAGTTTTTGGTCTTACCCCAACCCAATACCCAAAAGGTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATAAAATTTTGACATAACCAAATATTATTTTCCGCCACGAATTGAGTCTACGAGAGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATAAAATTTTGACATAACCAAGTATTATTTTCCGCCACGAATTGAGTCTACGAGAGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGCTTTTAAATTTGGGAAAATTTAATAATAATATGTATTAAATGGACAAATAAAAGTTAG
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pesvygdegdkpqmrmrrttfteiassyddvnatksqrnpnglpnpshrrisggsda
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99.1%;
                            103223 bp
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Pred. No. 7e-94;
                                                         103223
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                                                         PLN 30-OCT-2002
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VERSION
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SOURCE
ORGANISM
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REFERENCE
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AUTHORS
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JOURNAL
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                                                                                   misc_teature
                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                Genes with similarity to proteins in the databases are described as putative, '-like' or 'similar to'. Genes that have EST similarity but no significant protein similarity are described as 'unknown proteins'. Genes that are annotated based only on gene prediction software are described as 'hypothetical proteins'. The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/section/index.html), GENSCAN (Chris Burge, http://gnomic.stanford.edu/~chris/GENSCANW, html), Fexa (V.Solovyev & A.Salamov, Sanger Centre, http://genomic.sanger.ac.uk/), and NetPlantGene (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/NetPlantGene.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
On Apr 9, 1999 this sequence version replaced gi:4508084.
Bases 1-33654 of clone of clone F3F20 overlap with bases 50550-84203 of 'TAMU' clone T25N20, gb|AC005106.
e-mail for correspondence: arabbasequence.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (17-MAY-1999) DNA Sequencing and Technology Center,
Submitted University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Huizar, L., Rowley, D., Buchler, E., Dunn, P., Gonzalez, A., Kremenetskaia, I., Kim, C., Lenz, C., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vyotskaia, V., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (08-APR-1999) DNA Sequencing and Technology Center,
Submitted University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rederspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Huizar, L., Rowley, D., Buehler, E., Dunn, P. Gonzalez, A., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vyotskaia, V., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F. Altafi, H., Araujo, R., Huizar, L., Rowley, D., Buchler, E., Dunn, J. Gonzalez, A., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S. Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vysotskaia, V.S., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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AC007153.2
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/note="overlap with bases 50550-84203 of 'TAMU' clares from bases 1 to 29,00 annotated on overlapping clone T25N20, gb|AC005106
                                                                                                                                                                                                 organism="Arabidopsis"
/mol_type="genomic_DNA"
/cultivar="Columbia"
                                                                                                             /clone="F3F20"
                                                                                                                                          /db_xref="taxon:3702"
/chromosome="I"
                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
                                                                                         .33654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GI:4580365
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Liu, S.,
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/gene="F3F20.1"
/gene="Farefale.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /proteIn_id="AAD30611.1"
/db_xref="G1:4836909"
/db_xref="G1:4836909"
/translation="MESNGGGEVRRYNLVYFLSRSGHVDHPHLLRVHHLSRNGVFLR
DVKKWLADARGDAMPDAFSWSCKRRYKNGYVWQDLLDDDLITPISDNEYVLKGSEILL
SSPKEDYPNVEKKAWVTRNGGIDAEEKLQKLKLTSEKIQKESPVFCSQRSTATTSTVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WMEKELEHLAHSGYRGITLEIFLALRFFIFQYGLVYHLSTFKGKNQSFWYYGASWFVI
LFILLIVKGLGYGRRRFSTNFQLLFRIIKGLVFLTFVAILITFLALPLITIKDLFICM
LAFMFFGWGMLLIAQACKFLIQQLGIWSSVRTLARGYEIVMGLLLFTPVAFLAWFPFV
SEFQTRMLFNQAFSRGLQISRILGGQRKDRSSKNKE"
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/note="Highly similar to putative callose synthase catalytic subunit; Highly similar to cotton putative callose synthase catalytic subunit, gb|AAD25952"
                                     complement (join (47118. .48467, 48761. .49149, 49186. .49302
                                                                                                                                                                                                                  EESTTNEEGFVLKKQDPKTVSGQRDGSTENGSGNDVESGRPSVSSTTSSSSYIKNKSY
SSVRASHVLRNLMKCGGLDTNDAVLVPLNKSRSGAFGPAWEDERRYQYHQQHNARKSF
EGAWGGIKMKETIEFCKPKVAPSKPSWAPLCSQCGKLFKPEKWHSHMKLCRGMKNSSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (join (44167. .44362,44438. 45331. .45446,45524. .45593,45680. .
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LRFWEBCLCYI YHHLY CMLAGSVS PMTGEHVKRAY GGEDEAFLQKVVTP I YQTI SKEA
KRSRGGKSH4SVWRNYLDLNIX YWSLI ROFRLCWPMRADAD FFCOTAEELALERSEI KS
NSGDRWMGKVNF VE I RS FWH I FRS FDRLWS FY I LCLQAMI V I ANNGSGELSAI FQGDV
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EDVEVADEVNLIVDIDLIKTQIYVPYNILPLDPDSQNQAIMRLPEIQAAVAALRNTRG
LPWTAGHKKKLDEDILDWLQSMFGFQKDNVLNQREHLILLANVHIRQFPKPDQQPKL
                                                                                                                                                                             NNDLMTSNNTVKPROORCRNIPGNPLGHORVLTTTLKE"
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ILITVSIWFMVVTWLFAPFLFNPSGFEWQKIVDDWTDWNKWIYNRGGIGVPPEKSWES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="F3F20.2"
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ILRVANEVEASNPRVAYLCRFYAFEKAHRLDPTSSGRGVRQFKTALLQRLERENETTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAD30609.1"
/db_xref="GI:4836907"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="Hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="F3F20.2"
.49979,50064. .50318))
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.45812))
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                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                 ATGAGAGTTTTTTAAATTTTTATTATAAAATAA-TTTTTTGCATGAAATTGTTTTTAA 118
                                                                                                                                                                                                                                                                                        AAGCTTTTAAATTTGGGAAAATTTAATAATATATGTATTAAATGGACAAATAAAAGTTAG
                                                                                                                                                                                                                                                                                                                   AAGCTTTTAAATTTGGGAAAATTTAATAATATATGTATTAAATGG-CAAATAAAAGTTAG 59
                                                                                              GATAAAATTTTGACATAACCAAATATTATTTTCCGCCACGAATTGAGTCTACGAGAGATG 20345
                                                                                                                                          GATAAAATTTTGACATAACCAAGTATTATTTTCCGCCACGAATTGAGTCTACGAGAGATG 178
TCCTGTCTTTAAA-CTCGTAAAGTTTTGGTCTTACCCCAACCCCAATACCCACAAAGGTAAA
                                            TCCTGTCTTTAAACCTCGTAAAGTTTTGGTCTTACCCAACCCAATACCCACAAAAGGTAAA 238
                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TDLCTWVLLVFGFASFSKSGTWNKMMPFVIITTAIFVLLCIFVIRFGIAWIFAKTVKA
GGVVLCGLITDACGVHSITGAFLFGLSIPHDHIIRMIEEKLHPLGSILMPLFYIIG
GLRADIGFMLGPTDKFMWVVVLCSSFLVKIVTTVITSLFMHIPRDAFAIGALMNTKG
GLRADIGFMLGPTKKALDSPMYTHMTIALLVMSLVVEPLLAFAYKPKKKLAHYKHRTVQ
KIKGETELRVLACVHVLPNVSGITNLLCVSNATKGSPLSVFAHLVELTGRTTASLLI
MNDECKPKANFSDRVARESDQIAETFERAMESUNDAMTVGTITAVSPYATMHEDICVLA
EDKRVCFIILPYHKHLTDDGRMGEGNSSHARINQNVLSHAPCSVGILVDRGMAWVRSB
SFRGESNKREVAMLFVGGPDDREALSYAWRMVGOHVIKLTVVRFVPGREALISSGKVA
AEYEREKQVDDECIYEFNTMNDSSVKYIEKVVNDGQDTIATIREMEDNNSYDLYVV
GRGYNSDSPVTAGLNDWSSSPELGTIGOTLASSNFTMLASVLVIQQYSARKQAAVTA
AAATTVMGAVAGVTGNNLESAGGDAKMTRDAHEPFMKSMYEDEDEDDEEDHQYGIHR"
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STLASSLPFFITQLFVANLSYRVLYYLTRPLYLPPFVAQILCGLLFSPSVLGNTRFII
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/note="similar to Na/H antiporter proteins; N-terminal
half of protein is similar to Na/H antiporter proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /proteIn_id="AAD30626.1"
/db_xref="GI:4836924"
/translation="MSVYMPRVLTPSLLSQILKKOKNPVTALKLFEEAKERFPSYGH
NGSVYATMIDILGKSNRVLEMKYVIERMKEDSCECKDSVFASVIRTFSRAGRLEDAIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53685. .55199
/gene="F3F20.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Similar to hexosaminidase; Similar to
hexosaminidase, gi|1170249, gi|1076942 and others"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AHVFPYRFTMVLETFANLALVYNIFLLGLGMDLRMVRITELKPVIIAFTGLLVALFVG
AFLYYLPGNGHPDKIISGCVFWSVALACTNFPDLARILADLKLLRSDMGRTAMCAAIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="Hypothetical protein"
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/db_xref="GI:4836908"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon_start=1/
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99.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                     Score 653.8; DB 8
Pred. No. 6.7e-94;
                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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20404
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239 CGACCATACCGGTTAATAATATTCTAACCGGTTTATAAGTTTACATAAATCATTTACTAA 298

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REFERENCE
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Homo sapiens chromosome 8, clone CTD-2017M22, complete sequence.
AC093566
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RS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Boyukly,L., Boukhgalter,B., Brown,A., Chargata,J., Chargotiano,A., Charg,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Choepel,Y., Colangelo,M., Gollins,S., Collymore,A., Cook,A., Choepel,Y., Colangelo,M., Galagan,J., Gardyna,S., Farceira,P., FitzHugh,W., Galagan,J., Gardyna,S., Farceira,P., FitzHugh,W., Graham,L., Gardyna,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamata,A., Kells,C., LaRocque,K., Liu,G., MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C., Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J., McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Neddrim,J., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., O'Ne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (29-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Nov 13, 2001 this sequence version replaced gi:16041411. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
Center project name: L12730
Center clone name: 2017_M_22
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complement(4057. .4520)
/rpt_family="L1MCb"
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                                                                                                                                                        complement (7834. .8206)
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106. .781
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:al Similarity 46.5%;
236; Conservative
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                                                                                        AF217246.5 GI:14327861
HTG; HTGS PHASE1; HTGS DRAFT; HTGS CANCELLED.
Homo sapiens (human)
Homo sapiens
                                                                                                                                                      174080 bp DNA linear HTG 26-JUL-2002
Homo sapiens chromosome 8 clone CTD-2017M22 map 8q24, WORKING DRAFT
SEQUENCE, 20 unordered pieces.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 174080)

Schilhabel,M.B., Baumgart,C., Blechschmidt,K., Dette,M., Jahn,N., Lehmann,R., Menzel,U., Polley,A., Reichwald,K., Schudy,A., Siddiqui,R., Taudien,S., Wen,G., Rosenthal,A. and Platzer,M.
                                                                                                                                                                                                                                                                                 CATGTATATATATATATATATTGTA 87266
                                                                                                                                                                                                                                                                                                          AATATAGAAAGTGAACAAAAAAATTA 511
                                                                                                                                                                                                                                                                                                                                        TIGTATATGTTTTACATGTGTAATATATATATATATTGTATATGTATATGTTTTACATGTATAAT 87179
                                                                                                                                                                                                                                                                                                                                                                                                                       TAGTACTTGTTTTTTGGGTTCAACTAGTTACTTTTTTCCTTTGACATCAAAATT
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33826. .3
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32015. .3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="AT_rich" 33914. .33969
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/rpt family="L1MC2"
complement(30049. .30160)
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/rpt_family="MIR"
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244

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86879

64

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JOURNAL REFERENCE
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany On Jun 7, 2001 this sequence version replaced gi:9967152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence Quality Assessment:
This entry has been annotated with sequence quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Taudien, S., Wen, G.P., Schilhabel, M., Menzel, U., Jahn, N., Baumgart, C. and Rosenthal, A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (16-DEC-1999) Genome Analysis, Institute of Molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chromosome 8 genomic sequence Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Base-by-base quality values are not generally visible GenBank flat file format but are available as part of this entry's ASN.1 file.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number wil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               be preserved.
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1004
10220
10320
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Consensus quality: 114626 bases at least Q40
Consensus quality: 155148 bases at least Q30
Consensus quality: 165205 bases at least Q20
Quality coverage: 4.37 x in Q20 bases; sum-of-contigs
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Center clone name: CTD-2017M22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://genome.imb-jena.de/
Contact: gscj-submit@genome.imb-jena.de
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10219:
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contig of 9216 bp in length
gap of unknown length
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of 6973
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of 3515
                                                                                                                                                                                                                                                                            unknown length
of 3396 bp in length
unknown length
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             of 13860 bp in unknown length
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VERSION KEYWORDS

ACCESSION

DEFINITION

Danio rerio clone CH211-59L22,

186175 bp

SEQUENCING

linear HTG 06-MAR-2004 ING IN PROGRESS \*\*\*, 16

POCUS

CR318664

SOURCE

ORGANISM

Danio rerio (zebrafish) Danio rerio CR318664.4 GI:45238492 HTG; HTGS\_PHASE1. unordered pieces. CR318664

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii; Neopterygii; Teleostei; Ostariophysi

Ostariophysi;

Euteleostomi;

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RESULT 5
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Best Local Similarity
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                                                                   TACATGTATAATATATATATAGTA 171278
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                                                                                                                                   ATATAÄTATATTGTATATGTTTTTACATGTATÄÄTATATATÄTÄTATTGTÄTATGTTT 171305
                                                                                                                                                                                                   TTGTATATGTTTTACATGTGTAATATATATATATATTGTATATGTTTTACATGTGTAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATATAGAAAGTGAACAAAAAAAATTA 511
                                                                                                                                                                ATTGTAGACGAGTGGTCCATATATAGATGGTGAAATGAAATGAATATTGAGTAATAAATA 484
                                                                                                                                                                                                                                  TAGTACTTGTTTTTCTTTTTGGGTTCAACTAGTTACTTTTTTCCTTTGACATCAAAATT
                                                                                                                                                                                                                                                                  TGTAATTAAGTTTTATGAAATGTGGTTATTTTGTAGGTCACGTGAAATTTATTAATTTTT 364
                                                                                                                                                                                                                                                                                                                                                                                                    ATATTCTATATGTTTTATATGTATAATATATATATATATTCTATATGTTTTATATGTAT 171545
                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTTAAACCTCGTAAAGTTTTGGTCTTACCCAACCCAATACCCACAAAGGTAAACGACCA 244
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1170976
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/clone="CTD-2017M22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="8"
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124140: contig of 16448 bp in length
124240: gap of unknown length
149239: contig of 24999 bp in length
149339: gap of unknown length
170975: contig of 21636 bp in length
171075: gap of unknown length
172471: contig of 1396 bp in length
172571: gap of unknown length
172571: gap of unknown length
172670: gap of unknown length
17480: contig of 1509 bp in length
17490: contig of 1509 bp in length
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Pred. No. 0.013;
0; Mismatches 272;
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COMMENT
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                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
misc_feature
                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Mar 7, 2004 this sequence version replaced gi:45126687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chemistry: Dye-terminator; 100% of reads consensus quality: 180247 bases at least Q40 consensus quality: 180993 bases at least Q30 consensus quality: 181829 bases at least Q20 consensus quality: 181829 bases at least Q20 Insert size: 184675; sum-of-contigs Insert size: 184675; sum-of-contigs Quality coverage: 8.23x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center project name: zC59L22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
----- Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (04-MAR-2004) Wellcome Trust Sanger Institute, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McLay, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 186175)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coverage: 7.74x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Assembly program: XGAP4; version 4.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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166951
183316
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                                            /organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
                              <u>`c</u>1
              /clone
                                                                                            .186175
                 .one="CH211-59L22"
.one_lib="CHORI-211"
                                                                                                                                 136627: gap of 100 bp
166850: contig of 30223 bp in length
166950: gap of 100 bp
183315: contig of 16365 bp in length
183415: gap of 100 bp
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contig of 16602 bp in length
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of 13500 bp in length
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of 3228 bp in length
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ACCGGTTAATAATATTCTAACCGGTTTATAAGTTTACATAAATCATTTACTAATCCGCGT 305
                                                                         TTTAAACCTCGTAAAGTTTTGGTCTTACCCCAACCCAATACCCACAAAGGTAAACGACCAT 245
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136628. 166850
/note="assembly_fragment:01736
/----ment_chain:2"
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/note="assembly_fragment:00754
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/note="assembly_fragment:00149
fragment_chain:1"
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fragment_chain:2"
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ragment_chain:1"
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ragment_chain:1"
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ragment_chain:1"
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ragment_chain:2"
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ragment_chain:2"
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ragment_chain:2"
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ragment_chain:2"
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ragment_chain:1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Assembly program: XGAP4; version 4.5 Chemistry: Dye-terminator; 100% of reads Consensus quality: 243112 bases at least Consensus quality: 243477 bases at least Consensus quality: 243996 bases at least teast programmer and the second 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Insert size: 24589; sum-of-contigs
Insert size: 241608; 2.3% error; agarose-fp
Quality coverage: 7.87x in Q20 bases; sum-of-coverage: 8.07x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Wellcome Trust Sanger Institute Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (21-MAY-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Danio rerio (zebrafish)
Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: zK2J6
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1. (bases 1 to 246589)
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                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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8: contig of 28228 bp in length
8: gap of 100 bp
7: contig of 11119 bp in length
7: gap of 100 bp
4: contig of 9327 bp in length
4: gap of 100 bp
1: contig of 48577 bp in length
1: contig of 66893 bp in length
1: gap of 100 bp
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209127: contig of 14270 bp in length
209227: gap of 100 bp
224943: contig of 15716 bp in length
225043: gap of 100 bp
230389: contig of 5346 bp in length
230489: gap of 100 bp
236916: contig of 6427 bp in length
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236916: contig of 6427 bp in length
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Homo sapiens clone RP11-678P10,
                                                                                                                                                                                                                                                             Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Jul 13, 2000 this sequence version replaced gi:6554520.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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NOTE: This record contains 163 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads
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                                                                                                           Contact: sequence submissions@genome.wi.mit.edu
----- Project Information
Center project name: L4327
                                                                                         Center project name: L4327
Center clone name: 678_P_10
                                                                                                                                                                                Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                      Center code: WIBR
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and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that
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AL929359 AL844508
AL929359.1 GI:23505209
                Squares, S., Stevens, K., Tay Whitehead, S., Woodward, J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 419 (6906),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="UniProt/TrembL:Q812K2"
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LPNDHEKSNENALPYDNMKLDKDEYPNPPIKSHEQDCCSDKSFDECARKKELELNNNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Moderate similarity to Mus musculus unknown TR:AAH06701 (EMBL:BC006701) (297 aa) fasta scores: 0.028, 28.962% id in 183 aa. ProfileScan hit to PS: Ubiquitin-associated domain."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KNYDIYNENAEESNNYSSPYNKKYRLIGDFSRYMSVTINEKKGGLHNNCTTVLVDVD
LFPNVSENYLSKMFDYLTNFKDEEINKNE
Join (337. .3354,3499. .3577,3792. .4561)
/gene="PFI1525w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db~xref="UniProt/TremBL:Q812K1"
/translation="MDEENKLVEQLVEMGYSKEISQKVIQKSGAKTIEDAISWIELLD
ETENMTDEELKDVNTKDEEKGDSFKNKEKLKSENDMDENNITSCEKMSKLSPEEAQKK
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NYKFLHIKRKLNCLFIRNNITDIRNLKYLTYKKVIQFKKDMNICLSEAYNSFDYKNKK
                                                                                                                                                                                                                                                          HMM (Signal peptide probabilty 0.005, signal anchor probability 0.937) with cleavage site probability 0.004 between residues 28 and 29
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EHKKEKEKOLELLKREYEAKFGI EYKI GNEKKKLODL TENEKADEI A LLFUNLKKNYK
DTKKOELLASLUI LRTYFSNI YDNI LEKKYOKI KKENKI FVEKI KI FEEMLHI FLLVG
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complement(13072...13920)
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DYLLSLYFKGELKKDQIIIQPKEAFCIKTKILYSNQTSIQNICFENAGSGSVGIPYSL
SQIRPDKYGNNMSCLSIDCCVNPFTIDVIRKYNEVFNFMLEDVCLNIEKNIMKDKERI
CRDFKMLSNMKCKGEKPFLLCINKNVLKKNILLEEEKKLEKLKKEYEEKNETSKDVDN
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NPNBEFINLSEDIKKMEIKDPNYLQCILYTLHL"
join(10145. .10388,10425. .10511,10701. .12151,12317. .126
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lksrgylskedfysthyokkkknekniikeekvnniiydinllynnskofffnlnyhl
hfcoekkistilfiryiskkkseissyidinnkkiaekinkkkyiyaskkdlsyynwh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="proteasome precursor, putative"
/protein_id="CAD51995.1"
/db_xref="G1:23505215"
/db_xref="G1:23505215"
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KGRFHEGETIYDETTYDEEIDLDSINYLDYNNNDNNLVTKNKYFYEDKFNDYNPLVE
KVAHITKKIIYTNNNFLSCALIFGGYDKIKKQQLYAVNLNGSIIEKHDFAVSGGGSIN
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/db_xref="GI:23505214"
/db_xref="UniProt/TrEMBL:0812J8"
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/gene="PFI1540w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="hypothetical protein"
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/db_xref="UniProt/TrEMBL:Q812J9"
/db_xref="UniProt/TrEMBL:Q812J9"
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/gene="PFI1535w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           join(8267. .8365,8749. .9405)
/gene="PFI1535w"
                                                                                                                                                                                                                                                                                                                                            complement (join (15258. 16144. .16285))
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/codon_start=1
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/db_xref="GI:23505216"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="PFI1550c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16144. .16285)
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                                                                                                                                                                                                                                                                            gene="PFI1550c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lement (join (15258. .15314, 15535.
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TTTTTAGTACTTGTTTTTCTTTTTTGGGTTCAACTAGTTACTTTTTTCCTTTTGACATCAA 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TATATTTTTAATTATTTTATATTTTTTTTTTCTCTATAGAATAATTTTTTCATTGAAC 168177
                                                                                                                                                                                                                                                                                                                                                                                                                                    CGCGTGTAATTAAGTTTTATGAAATGTGGTTATTTTGTAGGTCACGTGAAATTTATTAAT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAATATATATATATAAATTAATA ----TTTTTAAAGCAACATATATTATTATAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGTCTTTAAACCTCGTAAAGTTTTGGTCTTACCCAAACCCAATACCCACAAAGGTAAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAATTATTCTATATATGAAAACAATAAAATAAATTATTTTTTTATTATATAAACAAAGTA 168413
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                                                                                                                            AATAAATATAGAAAGTGAACAAAAAAAATTAGTGGAAAAGGTAACT 526
                                                                                                                                                                                                                             AATTATTGTAGACGAGTGGTCCATATATAGATGGTGAAATGAAATGAATATTGAGTAATA 480
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join 17997. . 18035,18047. . 18112,18218. . 18278,18587. . 18845,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="UniProt/TremBL:Q812J6"
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YLFFLHRFRSMCCWIFASYFKENYLSFFCSFLDIFLCKHIICYFIIFFNSTECIKLQN
VNIILHIYIIYIYICATFYQKNK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(19209. .19255,19418.
23133. .23511))
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19040. .19172)
/gene="PFI1555w"
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/protein_id="CAD51997.1
/db_xref="GI:23505217"
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linear
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PRI 31-JAN-2004
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JOURNAL
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To cite this work please use: SeattleSNPs. NHLBI HL66682 Program
for Genomic Applications, UW-FHCRC, Seattle, WA (URL:
http://pga.gs.washington.edu).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens arachidonate 12-lipoxygenase (ALOX12) gene, complete
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Submitted (15-JAN-2004) Genome Sciences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 18556)
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join(1980. 2114,2688. 2889,4372. 4453,4578. 4700,
4816. 4919,5169. 5329,6199. 6342,7465. 7674,11122. .
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EEEEFDHDVAEDLGLLQFVRLRKHHWLVDDAWFCDRITVQGFGACAEVAFFCYRWVQG
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  <u>EDILSLPEGTARLPGDNALDMFQKHREKELKDRQQIYCWATWKEGLPLTIAADRKDDL</u>
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|mol_type="genomic DNA"
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RQCWQDDELFSYQFLNGANPMLLRRSTSLPSRLVLPSGMRELLRAQLEKELQNGSLFEA
DFILLDGIFANVIRGEKQYLAAFLVMLEMEPNGKLQPWVIQIQPENBSSFTPTLFLPS
DPPLAWILAKSWYRNSDFQLHEIQYHLLNTHLYAEVIAVATWRGCLPGLIPIFEKFLIPH
IRYTMEINTRAKTQLISDGGIFDKAVSTGGGGHVQLLRRAAAQLTYCSLCPPDDLADR
GLLGLFQALYAHDALRLMEIIARYVEGIVHLFYQRDDIVKGDPELQAWCREITEVGLC
QAQDRGFPVSFQSQSQLCHFLIMVGTCTAQHAAINQGQLDWYAWPDNAFCTWRMPDP
TYKEDVIMATVMGSLPDVRQACLQMAISWHLSRRQPDMVPLGHKEKYFSGPKPKAVL
NQFRTDLEKLEKEITARNEQLDWPYEYLKPSCIENSVTI"
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/frequency="0.07"
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                          gene="ALOX12"
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                                                                                                                                                                                                                                                                                      /gene="ALOX12"
/frequency="0.36"
/replace="c"
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                                                                                                               Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cook, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Cook, A., Cook, P., FitzGerald, M., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Graham, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Graham, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Graham,
Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaR Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Lindbla
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (11-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 174741)
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Lindblad-Toh,K.,
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Research, 320 Charles Street, Cambridge, MA 02141, USA CE 4 (bases 1 to 174741)

Example of the content of the 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (19-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 15, 2002 this sequence version replaced gi:21307465. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
Center project name: L9393
Center clone name: 589_P_10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
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                                                                                                                                   complement(31462. .31759)
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RESULT 11
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Danio rerio clone DKEY-178N6, *** SEQUENCING IN PROGRESS ***, 7
                                                                          Submitted (07-OCT-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquirite: Cfish-help@sanger.ac.uk Clone requests clonerequest@sanger.ac.uk On Oct 9, 2004 this sequence version replaced gi:53850225.
                                                                                                                                                                                                                                                                                                          CR847887
CR847887.2 GI:54019808
                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 225328)
                                                                                                                                                                                                                                                                     Danio rerio (zebrafish)
                                            Center: Wellcome Trust Sanger Institute Center code: SC
                                                                                                                                                                                                                                                                                         HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                          unordered pieces.
Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
----- Project Information
                                                                                                                                                            Direct Submission
                                                                                                                                                                              Sims,S.
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complement(33249...33789)
/rpt_family="LLMD2"
complement(33791...35118)
/rpt_family="L1PA13"
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Pred. No. 0.054;
0; Mismatches 2
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Insert size: 220016; 4.5% error; agarose-fp
Quality coverage: 9.09x in Q20 bases; sum-of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project name: zK178N6
GTTTTTTTAAATTTTTTATTATAAAATAATTTTTTGCATGAAATTGTTTTTAAGATAAAA
                                                                       arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                          TTTAAATTTGGGAAAATTTAATAATATATGTATTAAATGGCAAATAAAAGTTAGATGAGA
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ilarity 36.3%;
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217433. .225328
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fragment_chain:2"
178709. .217332
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fragment_chain:1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-178N6"
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fragment_chain:2"
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Eragment_chain:2"
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fragment_chain:1"
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fragment_chain:1"
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217332: contig of 38624 bp in length
217432: gap of 100 bp
225328: contig of 7896 bp in length.
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128865: contig of 3815 bp in length
128965: gap of 100 bp
178608: contig of 49643 bp in length
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2752: gap of 100 bp
1362: contig of 108610 bp in length
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of 13488 bp
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                                                                                                                                                                                                                                  Direct Submission
Submitted (07-0CT-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 ISA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Oct 9, 2004 this sequence version replaced gi:53828279.
Assembly program: XGAP4; version 4.5 Chemistry: Dye-terminator; 1100% of reads Consensus quality: 15049 bases at least Consensus quality: 160501 bases at least Consensus quality: 161321 bases at least Insert size: 164397; sum-of-contigs Insert size: 191089; 11.8% error; agarose
                                                                                                                                                      Center: Wellcome Trust Sanger Institute Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
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Danio rerio
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                                                                                                                                           Center project name: zKp115D7
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SEQUENCING IN PROGRESS ***, 15
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77556. .80989
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fragment_chain:1"
                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Danio rerio"
/mol_type="genomic DNA"
              /note="assembly_fragment:00229
fragment_chain:3"
84587..87803
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fragment_chain:1"
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note="assembly_fragment:00185"
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fragment_chain:2"
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_xref="taxon:7955"
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125230: gap of 100 bp
165797: contig of 40567
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AX4, complete sequence.
AC115599
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fragment_chain:4"
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125231. .165797
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109843. .114805
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                                                              125623 bp
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2 map 4229098-4354721 strain
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Direct Submission
Submitted (21-MAR-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany
3 (bases 1 to 125623)
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Dictyostelium discoideum

Dictyostelium discoideum

Dictyostelium discoideum
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Gloeckner,G., Elchinger,L., Szafranski,K., Pachebat,J., Dear,P., Lehmann,R., Baumgart,C., Parra,G., April,J.F., Guigo,R., Kumpf,K Tunggal,B., Cox,E., Quail,M.A., Platzer,M., Rosenthal,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (http://genome.imb-jena.de/dictyostelium/)
and the Univerity Colonge, Institute for Biochemistry I
(http://www.uni-koeln.de/dictyostelium/project.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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                                                                                                                                                                                                   /protein_id="AAL92328.2"
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/db xref="G1:28828944"
/db xref="G1:28828944"
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/transl ation="FKGNQKOQVNALLSQIYOGNIFSTEPFNFINGKMNDQIPE
FTGVPVTLTVDFSVFEDLTYFISSSAISFSPNIFSRLPNFFSPEVYFNIGKMNDQIPE
DIVLPENLYTVEFKSISVPLPNAFFSTGAIGTILINNANFGFALLPNGFPONNFLKQLN
LNIIGNGFPESNAGSALSNLTELTLNINNYNTMNITFPTFFEPFNGLTKLAINFHSADP
LNQLFEFEPTINNINFLEELHIENLGFNISNDVDLTNLSKNLKLTFSNHTILFLNKFKY
PLNCSLDLSNYPVSIYDVDFRNLTSLGSLSNNVYGENLPRANFDDFEKLTYLLLSSNQF
NGSLPESYCSFVKGSLALGSNDLTGSVDFDFDCFKLLGGEEFPGLFPNFDDFFDDTPADV
CTAFSLDVPVNQLLKTNGTTVFEFTGSNLGWDSDIESTQANVELAIIEPNKIKITIP
PGAGIQNATLKFGSNPSIEVLINYEFYGPTIDSYYVQGSGIFFRGSYFSYNQDYENIF
TINKDYKFTAHIQTIEDQNLNNGVGFENDDTPISVLKNREAFNVSIDVAGKGSETVTF
IYFGNITMLSDLSSIQLNTTGGDFSFTNEIKFIETFTFTFTFTFTFTFTSTSTST
INTYPPIENAGTYSLYIEVODFSFTNEIKFIETFFPFPTFTFTSTSTST
INTYPPIENAGTYSLYIEVODFSFTNEIKFIETFFPFPTFTFTSTSTST
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Location/Qualifiers
                                                                                          SDDEGLSTSPTLSISFIYLFSIILLINFVF"
Complement (join (3950. 4537, 4680. 4
/note="GeneID exon scores (in order
38.84, 6.50 - GSCJ_ID dd_00185"
/codon_start=1
/product="similar to Ralstonia solanacearum (Pseudomonas
solanacearum). Putative GST-related protein (EC 2.5.1.18)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /map="4229098-4354721"
join(<416. .688,837. .1349,1434. .1493,1638. .2931)
/note="GeneID exon Bcores (in order of location ranges):
10.12, 21.67, 1.80, 118.27 - GSCJ_ID dd_00183"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    product="similar to Dictyostelium discoideum (Slime
nold). Gp138"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mol_type="genomic
strain="AX4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Dictyostelium discoideum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            xref="taxon:44689"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Consortium
                                                                                                                     of location ranges):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kumpf, K.,
                                                                                                                                                                                                                                                                      SGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sd
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/product="similar to conserved hypothetical protein [Schizosaccharomyces pombe]"
/protein_id="AAL92333.2"
/db_xref="G1:2882897"
/translation="MRATHSRSVDVKTESTINIKTESTTKVKTESAIDRFKSKSKKTK
KHKKVYKSNSDNDDDHSNINNERKKVKKSITSLKNKKKPSKIKKDLEPVVDQRQRDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / trānslation="MLKSISLLKNNQILLKNIINNGRIINNVGEKLSKSLLKINYSS
STIDRTFNIIDCTIDKNSAEYKDNLINNNSTLKQLKENIEKIKGGGEKLNQKNISRG
KLLVBERIEALIDVGSFLEFSQLAGMGMYGKEEVAAGGIITGTIGKIHGVECVIVAND
ENVAGTYFFITVKKHLRAQEIAQENNLFCIYLVDSGGANLFRQADVFPDRDHFGRIF
ENQANNAKRIPQIAVVMGSCTAGGAYVPAMADESVIVKGTGTIFLGGFPLVKAATGE
IVTSEELGGADLHCRTSGVTDHYARDAEAIAITRRIVSGNLNRKKQPSFVUTTFTEEDI
YPTSELGGADLKNNFDIRKVIARLVDGSRFDEFKELYGTTLICGFARVHGMPVGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(9983. .11383)
/note="GeneID exon scores (in order of location ranges):
98.71 - GSCJ ID dd_00191"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IAIKDKSKTDILKEIYKFVGLDYEKSISTLLIFKMIINDKRTAKPNEFYNYSPPSETI
LIPIEFSDPELLKENHILLIQFGSFPIHRNRWPTKFTSTYNFFGTTEYFKYKGDFV
KIDRVKCPYVIDKFKSDFSIPQYGFTKYMGVPSEQITNFYSPSIRPEPCKPIVYHNDN
NNSERNATWLKLNFLLIFRYLGSRAVNDGRTVTYGEQLENLVSKDSSIEILEPLKDSI
NQSKCLICSRSTLSFGNFLCNTHYSKDLMDAFEKCKPYLFLDANNEPIKQLPKDQLES
/translation="MSIIYSPEVPFQLFEVELRDLDVNSEEFKFVAQIFNVGVPSTIK
KIQVVYNKSVMKNYNKNLGNSLKEIFVFHGSRLNEPKLIYTNGLLVEKTSAGLYFA"
                                                                                                                                                                                                                                                                                                                                                                KDI QS FKNSSKEVQYVVDNRDI ADLLVYF FKY FGY I FDYRNSMVN I LDYNNDKKEPMD
AEEELKFQNNREYDNKNHVLPLVDMKLGDTKDLF FI KDCI AGHNI TRCI LRSQLFTLI
                                                                                                                                                                                                                                                                                                                                                                                                                                   KRNDITKWCYQFSSILRANGFYNIKPIIHAKVPIVKFFDPKTEFHCDITLTKDSGNTG
VVKEFCQLLPILPVLIIFCKNWASVLNINDASQGTLSSYSITNMVIFVLQKKGLLPSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AKRAKELKYLEDNRVLEGENFYENVKLLETQTKKNYKLNGEILRKLSVDINKLSERVR
CYRDRTIILKRLEEVIKRETSLNKFGBIKVEIFGSSSTQLALKKSDVDIVMSFETELT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IANNGILFSESAVKGAHFIELCNQRGIPLVFLQNITGFMVGKTYESKGIAKDGAKMVM
AVATAKVPKITMIIGGSFGAGNYGMCGRSYSPRFLYMMPNAKISVMGGEQAASVLAQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FKENEKKKEKTVFIKDKFAYIDPSNLQSILDKKVKPYTQENNNYNYNSNYDDYY"complement(7921. .9687)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KYFQKAYLNLISGKLP" ·
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLSACMNQPINPPSDGFGVFRM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="mQnnkfdftIIndhkSpntykvelmLIELGVSYESISINDYLkN
NSNNRIPALIDNTFKVPNILYESGSVLIYLANKFSKLLPDFRLNATLQNNNSQIISKS
VWQLVNLIPSFNNNNNNNNNNNNNNNNNNNENEVKKVLQLLDDRLSTNQYLGGSQYSI
                                                                                                     /product="hypothetical protein"
/protein_id="AAL92334.2"
                                                                                                                                                                                                                 /note="GeneID exon scores (in 16.95 - GSCJ_ID dd_00194"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QKDNMAKENKQWSPEEENTFKKPISDKFEEEGSIYYSSARCWDDGVIDPQDSRKVIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="similar to Agrobacterium tumefaciens (strain / ATCC 33970). 3-methylcrotonoyl-CoA carboxylase beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="GeneID exon scores (in order of location ranges):
222.87 - GSCJ ID dd_00188"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              222.87 - GSCJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IVKKNSNLIGNKNIDNEKSNKVKEYPLKVKDSYTIHKDIGNNIVLYFKDKACNYQSDL
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/db_xref="GI:28828895"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/product="similar to Plasmodium falciparum (isolate 3D7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (5354. .7216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NLNNNGIKFSNDLGIAINAL"
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                                                                          db_xref="GI:28828898"
                                                                                                                                                                                   codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAL92331.2"
/db_xref="GI:28828896"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="AAO51485.1"
/db_xref="GI:28828894"
                                                                                                                                                                                                                                                                                                .13833
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                                                                                                                                                                                                                                                           order
                                                                                                                                                                                                                                                           of.
                                                                                                                                                                                                                                                       location ranges):
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CDS

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Matches 254;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTTGTTAAAATTTAAACCAATAGATTTTTATTAAAATCATAAAGATTATTTTGATTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTTTAAATTTTTTATTATAAAATAATTTTTTTGCATGAAATTGTTTTTAAGATAAAATTT 128
CCGGTTAATAATATTCTAACCGGTTTATAAGTTTACATAAATCATTTACTAATCCGCGTG
                                                                                                                                                                                       TTAAACCTCGTAAAGTTTTGGTCTTACCCAACCCAATACCCACAAAGGTAAACGACCATA
                                                                                                                                                                                                                                                                                          TCATCAAATAAAGTAATATTTTCCATATTATCAAAATAATAATCTAAAGATGTAAATCAA 27124
                                                                                                                                                                                                                                                                                                                                                                                    TGACATAACCAAGTATTATTTTCC--GCCACGAATTGAGTCTACGAGAGATGTCCTGTCT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAATTTGGGAAAATTTAATAATATATGTATTAAATGGCAAATAAAAGTTAGATGAGAGTT 68
                                                                                              TTTGAAATGGTGAATTATTTACAAAAAAATTCACATTAGAATATCTTTATCAAATCATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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/note="GeneID exon scores (in order
49.65, 142.60 - GSCJ_ID dd_00179"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MSVIINSIADLKTYEPTSTVTTVVVKAFTVNTNIGGGDFYYDSA
DTTTVTDNATVIVTNGGKRWKKVISDRUNTHFGALKDGVTDCSAACITMHWSVK
YAPKLGIRFPAGTFKISGIDLSNGTIAHFRMTGSTVAYGYFPATTLISDQGTGMWKV
KARWTEISNLIYGENBVKVNTKGFYQNTEIBEGFIRITNINFRNLGGVCVSKVDTLD
TKIDQFYVTRCTGGVIYGTWSGSATGSWDHLTAVELTNNIQNCTGANIFDLQRCTQS
IIRNGWIEHSDSPGDLSNGGWVIEALSWEDCVWPLMLTFCRYXITOKNLQGTSAILTN
DSTKSTWLS HENGGFEIENVGITTTGSMNYGOLTSEFRFSNSSASSQMLRILGEFFP
SDGDTLNIRIVGSLYIKLGFYVMNTVAILETSARDRYYAGVCRWYDGTKLDEFTA
DSTKJTHANTNCSIYIKLGFYVMNTVAILETSARDRYYAGVCRWYDGTKLDETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MNKILSILLISILILFILRVESYPTYGGSNSANIREDRHSFRA
pplQsGTGILYWDIEGSTIVNDDFIRLTSDQKSLHGAIWNTEPMEQPWWEVVFEFRY
GAGRIGADGIALMLUNRKEGNSQDFSIYGSKNLWKGLAIIFDTFDNDQNGDHPLISVF
YNDGTKFYETAKDGSNMKLGSCSSRYRNDKHNAKSRIRYYHGLLSVEIDPNGSGIFEK
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dpsliytnglraektqsglyfaiksesngftykntdcsqificriliprqnvsprfhv
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/protein_id="AAL92336.2"
/db_xref="GI:28828900"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="GeneID exon scores (in order of location ranges):
6.32 - GSCJ_ID dd_00190"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="similar to Erwinia amylovora, Amylovoran biosynthesis protein amsF precursor" /protein_id="AAO51487.1" /protein_id="AAO51487.1" /protein_id="GI:28828901" /procein_id="GI:28828901" /procein_i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="hypothetical protein"
/protein_id="AAL92335.2"
/db_xref="GI:28828899"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="GeneID exon scores (in order of location ranges):
6.39 - GSCJ_ID dd_00176"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VTTIEGIVQALPQASWNAGKNGIAIGSDGYFGITTVPIGTDNQLPIYINGSLYKIAVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="GeneID exon scores (in order of location ranges):
169.96 - GSCJ_ID dd_00184"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21628.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .20217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 67; DB 3;
Pred. No. 0.078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3; Length 125623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of location ranges):
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                                                                                                                                                                                                                                                                                                                                                                                  Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
CConsensus quality: 143152 bases at least Q40
CCOnsensus quality: 144900 bases at least Q30
CCOnsensus quality: 145119 bases at least Q20
Insert size: 147694; sum-of-contigs
Insert size: 147694; sum-of-contigs
Oquality coverage: 10.33x in Q20 bases; sum-of-contigs Quality coverage: 10.81x in Q20 bases; agarose-fp
Coverage: 10.81x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (03-SEP-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: clinerequest@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Sep 4, 2004 this sequence version replaced gi:51870356.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pieces
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Danio rerio clone CH211-276D21,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
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                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is
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be preserved.
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28744
28844
32354
32454
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                                                            2608: contig of 2608 bp in length
2708: gap of 100 bp
28743: contig of 26035 bp in length
28843: gap of 100 bp
32353: contig of 3510 bp in length
32453: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             name: zC276D2
contig of 12534 bp in length gap of 100 bp contig of 2045 bp in length
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Ostariophysi;
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NCE, 8 unordered
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GTCCATATATAGATGGTGAAATGAAATGAATATTGAGTAATAAATAAATATAGA-AAGTG 497
                       AAGTTTTGGTCTTACCCAACCCAATACCCACAAAGGTAAACGACCATACCGGTTAATAAT
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                                               CTTTTTTGGGTTCAACTAGTTACTTTTTTCCTTTGACATCAAAATTATTGTAGACGAGTG
                                                                                               ATGAAATGTGGTTATTTTGTAGGTCACGTGAAATTTATTAATTTTTTAGTACTTGTTTTT
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fragment_chain:3"
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79124. .<mark>13</mark>1483
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Fragment_chain:3
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fragment_chain:3"
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ragment_chain:2"
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ragment_chain:2"
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fragment_chain:1"
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|mol_type="genomic DNA"
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79023: contig of 31791 bp ir
79123: gap of 100 bp
131483: contig of 52360 bp ir
131583: gap of 100 bp
148394: contig of 16811 bp ir
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lone="CH211-276D21"
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Pred. No. 0.081;
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Chemistry: Dye-terminator; 100% of reads
Consensus quality: 193114 bases at least Q40
Consensus quality: 193781 bases at least Q30
Consensus quality: 194189 bases at least Q20
Insert size: 195862; sum-of-contigs
Insert size: 195862; sum-of-contigs
Outlity coverage: 6.5x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
------ Project Information
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
Danio rerio (zebrafish)
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----- Summary Statistics
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                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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5760: contig of 5760 bp in length 5860: gap of 100 bp 20214: contig of 14354 bp in length 20314: gap of 100 bp 34680: contig of 14366 bp in length 34780: gap of 100 bp 43318: contig of 8538 bp in length 4348: gap of 100 bp 73425: gap of 100 bp 73425: gap of 100 bp 109883: contig of 36458 bp in length
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Matches 242; Conservative
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fragment_chain:1"
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118156: contig of 8173 bp in length
118256: gap of 100 bp
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129172: gap of 100 bp
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Search completed: November 17, Job time: 3275 secs 2005, 16:54:19

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Minimum
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Abk28164 DNA trans	Abk39976 Human che	Aas45323 Chemicall	Adi72626 Human ova	Adl37765 Human ova	Acn56366 Cotton an	Adl44697 Human ova	Abl33407 Human imm	Acn53258 Cotton an	Ads89773 Oligonucl	Abq67075 Human ang	Ads89407 Oligonucl	Acn56344 Cotton an	Abv57072 Human pro	Acn61227 Cotton gy	Acn53258 Cotton an	Abk28418 DNA trans	Abk31493 Signal tr	Abl34061 Human imm	Aas45490 Chemicall	Abv10021 Human pro	Abl33688 Human imm	Acn51258 Cotton an	Adl38382 Human ova	Adi73251 Human ova

## ALIGNMENTS

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RESULT 1
ABZ10246/c
ID 246/c
ID 26202
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XX ABZ102
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XX Human;
KW Gene t
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XX Homo s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Berlin K, Braun A, Distler J,
Olek A, Piepenbrock C, Adorjan
Lewin A, Lipscher E, Maier S,
Schwope I, Ziebarth H;
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The present invention describes a method for detecting and differentiating between haematopoletic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a

Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides.

SEQ ID

NO 386;

117pp; English.

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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      which distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid. ABZ09861 to ABZ1118 represent specifically claimed nucleic sequences from the present invention. Oligonucleotides from the present invention can be used: for differentiating between healthy haematopoietic cells and proliferative disorder haematopoietic cells; for differentiating between acute
        19-SEP-2001
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                                                                       AAH71471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                       standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8056 BP; 3711 A; 0 C; 371 G; 3974 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TACCGGTTAATAATATTCTAACCGGTTTATAAGTTTACATAAATCATTTACTAATCCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTTTGACATAACCAAGTATTATTTTCCGCCACGAATTGAGTCTACGAGAGATGTCCTGT
                                                                                                                                                        AAATTAATAAAAAATAATTATTTTTT 6586
                                                                                                                                                                              TGGCTTGGCAAGATTCCATAAGTTTATTT
                                                                                                                                                                                                                     ÄÄTTTAATTÄAAAAÄTTTAAÄÄÄTTTCÄTATAAÄÄÄACATÄÄAAATÄÄÄÄACAÄTAAAATÄT
                                                                                                                                                                                                                                                     AATATAGAAAGTGAACAAAAAAATTAG-TGGAAAAGGTAACTGGAAAGAAAAGGCTTAT
                                                                                                                                                                                                                                                                                    ATTGTAGACGAGTGGTCCATATATAGATGGTGAAATGAAATGAATATTGAGTAATAAATA
                                                                                                                                                                                                                                                                                                                                                    TAGTACTTGTTTTTCTTTTTGGGTTCAACTAGTTACTTTTTTCCTTTGACATCAAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                   TGTAATTAAGTTTTATGAAATGTGGTTATTTTGTAGGTCACGTGAAATTTATTAATTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTTTAAACCTCGTAAAGTTTTGGTCTTACCCAAACCCAATACCCACAAAGGTAAACGACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAAAAAAATACAAAATAATTTTTTTTTTTTTTTTTAATTAAATCAATATATATTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGTTTTTTAAATTTTTTATTAAAATAATTTTTTTGCATGAAATTGTTTTTAAGATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTTAAATTTGGGAAAATTTAATAATATATGTATTAAATGGCAAATAAAAGTTAGATGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           allowing
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        (first
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                                                                       CDNA;
      entry)
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                                                                       612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 64.2; DB 8; Pred. No. 0.022;
                                                                                                                                                                                     572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 8056;
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RESULT 3
ABZ10246
ID ABZ1
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AC ABZ1
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ABZ10246 standard;

DNA;

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ВP

ABZ10246;

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Best Local S
Matches 136
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21-DEC-1999; 99US-0171350P.
14-MAR-2000; 2000US-0189315P.
12-MAY-2000; 2000US-0203791P.
09-UUN-2000; 2000US-0210600P.
21-UUL-2000; 2000US-0220114P.
                                                                                                                                                                                                                                                                                                                                   The invention relates to novel genes (AAH68727-AAH73383) associated with cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be useful for gene therapy
                                                                                                                                                                                                                                                                                                               Sequence 612 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200142467-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cervical cancer marker nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid for diagnosing and treating cervical cancer and for assessing and detecting compounds for treating the cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-DEC-2000; 2000WO-US033312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cervical cancer;
                                                                                                     145
                                                                                                                               371
                                                                                                                                                         205
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                         491
                                                                           431
                                                                                                                                                                                                                                    251
                                                   85
                                                                                                                                                                                                                                                              136;
                                                                                                                                                                                                                                                                         Similarity
                        GAAAGTGAACAAAAAAA 508
                                                                                                                                                                      TAAGTITTATGAAATGTGGTTATTTTGTAGGTCACGTGAAATTTATTAATTTTTTTAGTAC 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 564; 1051pp; English
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                                                                           GACGAGTGGTCCATATATAGATGGTGAAATGAATGAATATTGAGTAATAAATAAATATA 490
                                                                                                                                                                                                             TTTTTTTTTTNAAAATATTTTTTTGGTTTAGTTGAAATAATTGGGTATGGGTGTATTTT
                                                   TTGTTTTTCTTTTTGGGTTCAACTAGTTACTTTTTTCCTTTGACATCAAAATTATTGTA 430
                                                                                                                                                         TTAATAATATTCTAACCGGTTTATAAGTTTACATAAATCATTACTAATCCGCGTGTAAT
 AAAAAAAAAAAAAAA
                                                                                                     9.0%;
nilarity 52.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Deeds J,
                                                                                                                                                                                                                                                                                                               380 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytostatic; pre-malignant condition; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Berger
                                                                                                                                                                                                                                                                                                               50 C; 2 G; 178
                                                                                                                                                                                                                                                              °.
                                                                                                                                                                                                                                                                          Score 63.4;
Pred. No. 0
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                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                T; 0 U; 2
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                                                                                                                                                                                                                                                                                     DB 4;
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                                                                                                                                                                                                                                                              122;
                                                                                                                                                                                                                                                                                      Length 612;
                                                                                                                                                                                                                                                                                                                  Other;
                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                              0;
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16-JAN-2003

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Best Local S
Matches 274
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Olek A,
                                                                                                                                                                                                                                                                                                          determining the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) of haematopoietic cell proliferation disorder related sequences and their complements; and as primers for the amplification of haematopoietic cell proliferation disorder related DNA sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between subclasses, diagnosis, prognosis, treatment and/or monitoring of haematopoietic cell proliferative disorders. The present method enables highly specific classification of haematopoietic cell proliferative disorders allowing for improved and informed treatment of patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    represent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention can be used: for differentiating between healthy haematopoietic cells and proliferative disorder haematopoietic cells; for differentiating between acute lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         differentiating between haematopoietic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid. ABZ99861 to ABZ11118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent to distinguishes between methylated and non-methylated CpG dinucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; haematopoietic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaem cytosine methylation state; gene; ds.
                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a method for detecting and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-018942/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAR-2002; 2002WO-EP003401
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                                                                                                                                                                                                            Local Sir
hes 274;
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Piepenbrock C, Adorjan
Lipscher E, Maier S,
                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                             8056 BP;
ACATAACCAAGTATTATTTTCCGCCACGAATTGAGTCTACGAGAGATGTCCTGTCTTTAA
                                                                  TTTAAATTTTTTATTATAAAATAATTTTTTTGCATGAAATTGTTTTTAAGATAAAATTTTG 130
                                                                                                                                       ATTTGGGAAAATTTAATAATATATGTATTAAATGGCAAATAAAAGTTAGATGAGAGTTTT 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lipscher E, Ziebarth H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001US-0278333P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IJ
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                                                                                                                                                                                                                                                                             3711 A; 0 C; 371 G;
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                                                                                                                                                                                                            0
                                                                                                                                                                                                        Score 62.6; DB 8;
Pred. No. 0.043;
0; Mismatches 334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
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1 P, Grabs G,
Model F, Mu
                                                                                                                                                                                                                                                                             3974 T; 0 U; 0 Other;
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G, Lesche R,
                                                                                                                                                                                                                                         Length 8056;
                                                                                                                                                                                                            Indels
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New isolated nucleic acid molecule that encodes a plant protein or its fragment, useful for isolating a variety of agronomically significant genes associated with plant growth, quality or yield, and as molecular

WPI; 2004-479808/45.

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RESULT 4
ACN51594
                                                                                                                                                                                                                                                                          Cotton; plant; EST; expressed sequence tag; transgenic plant; androecium; variety Nucotton33B; library LIB3828; molecular tag; molecular marker; genetic mapping; molecular mapping; seed germination; plant growth; plant quality; plant yield; plant breeding; tissue printing; ss.
                                 (DEIK/)
(FENG/)
(FINC/)
(ZIEG/)
 Deikman
                                                                                                                                                                                                                                             Gossypium hirsutum
                                                                                                                                                                                                                                                                                                                                                              Cotton androecium tissue EST Clone ID: LIB3828-004-Q1-N6-H2,
                                                                                                                                                                                                                                                                                                                                                                                              02-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACN51594
                                                                                                                 14-DEC-2000; 2000US-0255619P
                                                                                                                                               12-DEC-2001; 2001US-00021323
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                                DEIKMAN J.
FENG P C C.
FINCHER K L.
ZIEGLER T E.
 <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GACGAGTGGTCCATATATAGATGGTGAAATGAATGAATATTGAGTAATAAATAAATATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGITITITCTITITIGGGITCAACTAGTTACTITITITCCTITIGACATCAAAATTATIGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAAGTTTTATGAAATGTGGTTATTTTGTAGGTCACGTGAAATTTATTAATTTTTTAGTAC 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCTCGTAAAGTTTTTGGTCTTACCCAACCCCAATACCCACAAAGGTAAACGACCATACCGG
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Feng
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA;
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   Fincher
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 Ziegler
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Claim 1;

SEQ

relates

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The

17880 cotton expressed sequence tags (ESTs; ESTs were isolated from cDNA libraries generated

ID NO 6375; 34pp; English

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RESULT 5
ABZ10100/c
ID ABZ10100 standard; D
XX
AC ABZ10100;
XX
DT 16-JAN-2003 (first
XX
DT 16-Jan-2003 eest
XX
KW Haematopoietic cell
XX
KW Human; haematopoieti
KW gene therapy; lympho
KW cytosine methylation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC molecular tags to isolate genetic regions, to isolate genes, to make the comparison of the control of the control of genes, to determine gene function and to determining whether genes are commenders of a particular gene family. The nucleic acid molecules may be used for isolating a variety of agronomically significant genes are compared with plant growth, quality, yield, and could also serve as colinks in metabolic and catabolic pathways. The nucleic acid molecules are collinks in metabolic pathways. The nucleic acid molecules are collinks in metabolic pathways. The nucleic acid molecules are collinks in metabolic pathways. The nucleic acid molecules are collinks in metabolic pathways. The nucleic acid molecules are colling seed germination or that may be used to mitigate stresses encountered colling seed germination. The ESTs additionally enable the acquisition of commoters and cis-regulatory elements which will be useful to express and also genetic and molecular mapping, and in cloning of agronomically schemes, genetic and molecular mapping, and in cloning of agronomically colling significant genes. The nucleic acid molecular are further useful for colling the expression level or pattern of a protein or mRNA and for colling the expression level or pattern of a protein or mRNA and for control variety Nucotton338 androceium tissue cDNA library (LIB3828). The sequence data for this patent did not form part of the printed control of the printed sequence as a specification in the printed secular sequence as a specification format directly from the US protein format directly from the US protein sequence as a specification in the printed sequence as a specification in the pri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Matches 144
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            gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia; cytosine methylation state; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 531
                                                                        Human; haematopoietic cell proliferation disorder; cytostatic;
                                                                                                                           Haematopoietic cell proliferation disorder related DNA sequence #240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             office at seqdata.uspto.gov/sequence.html?DocID=US20040123340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTTATGAAATGTGGTTATTTTGTAGGTCACGTGAAATTTATTAATTTTTTTAGTACTTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 13; Length 531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cc which distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118 cc represent specifically claimed nucleotide sequences from the present cinvention. Oligonucleotides from the present invention can be used: for differentiating between healthy haematopoietic cells and proliferative cd disorder haematopoietic cells; for differentiating between acute convention; the cytosine methylation state and/or single nucleotide convention; the cytosine methylation state and/or single nucleotide convention; the cytosine methylation state and/or single nucleotide convention of haematopoietic cell proliferation disorder crelated sequences and their complements; and as primers for the amplification of haematopoietic cell proliferation disorder related DNA sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between subclasses, diagnosis, prognosis, treatment and/or monitoring of haematopoietic cell proliferative disorders. The present method enables a chighly specific classification of haematopoietic cell proliferative disorders allowing for improved and informed treatment of patients
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent tidistinguishes between methylated and non-methylated CpG dinucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Berlin K, Braun A, Distler J, Guetig D, Berlin K, Piepenbrock C, Adorjan P, Grabs Lewin A, Lipscher E, Maier S, Model F, Schwope I, Ziebarth H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a method for detecting differentiating between haematopoietic cell proliferations associated with at least 1 gene and/or their regulatory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8056 BP; 3711 A; 371 C; 371 G; 3603 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            differentiating between haematopoietic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 28; SEQ ID NO 240; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-018942/01
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                                                                 1444 TTTTTTTTTTAAAAAAAAAAAATAAAAAATAAAAAAATCGATATTATTTTTATAA 1385
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245 TACCGGTTAATAATATTCTAACCGGTTTATAAGTTTACATAAATCATTTACTAATCCGCG
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                                                                                                                                              ATTITGACATAACCAAGTATTATTTTCCGCCACGAATTGAGTCTACGAGAGATGTCCTGT 184
                                                                                                                                                                                                                              ATTTTTTAAAAAAAATATTTTATTTAAAAAATTTTTTTAACGTATTTATATTTTTATATTTA 1505
                                                                                                                                                                                                                                                                                                            CTTTAAACCTCGTAAAGTTTTGGTCTTACCCAACCCAATACCCACAAAGGTAAACGACCA
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Pred. No.
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The invention relates to a nucleic acid comprising a sequence at least 18 CC bases in length of a segment of the chemically pretreated DNA of genes CC associated with pharmacogenomics according to one of the sequences of the genes ALDH6 (NM 00063), CYP1A1 (NM 000781), CYP1A1 (NM 000497), CYP3A3 (CC (NM 000776 and NM 017460), DPYD (NM 000110), EPHX2 (NM 001979), OCLN (CC (NM 001990, NM 019901, NM 019902, NM 019902, NM 019903, NM 019909) and CC their complementary sequences, or a sequence (S1) chosen from 87 CC sequences and their complements. The chemical pretreatment is bisulphite CC treatment to convert cytosines (but not methyl-cytosines) into uracils. CC peptide nucleic acid (PNA) -oligomer (II) in particular an oligonucleotide or a CC peptide nucleic acid (PNA) -oligomer, comprising in each case at least one base sequence having a length of 9 nucleotides which hybridises to or is concentrated with the methylation state (CC) analysing diseases associated with the methylation state (CC) analysing diseases associated with the methylation state (CC) analysing diseases associated with the methylation state (CC) and/or concentrated with the methylation state (CC) and/or state (CC) and (CC) an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 17; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid, oligonucleotides and peptide nucleic acid-oligomers, useful for detecting cytosine methylation state of genes associated with pharmacogenomics and for therapy of diseases e.g. cancer.
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01-SEP-2000; 2000DE-01043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oligomers may also be used as PCR primers. The set of 87 nucleic acid and their complements is useful for diagnosis and therapy of solid tumours and cancer. The present sequence represents one the 87 DNA sequences or its complement. Note: The sequence data for this patent not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11422 BP; 3867 A; 59 C; 1786 G; 5710 T;
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                          GCTTGGCAAGATTCCATAAGTTTATTT
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TATAGATTTAATATTTTATTTTATTT
                                                        AGTACTTGTTTTTTTTTTGGGTTCAACTAGTTACTTTTTTCCTTTTGACATCAAAATTA
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Pred. No. 0.
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antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antisporiatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer; disease; AIDS; epilepsy; acute myeloid leukaemia; Alzheimer; disease; AIDS; epilepsy; Human; immune system disease; cytosine methylation; antiasthmatic;

arthritis; psoriasis;

disease; gene;

Human immune system associated gene SEQ ID NO: 191.

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01-SEP-2000; 2000DE-01043826.
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The invention relates to 17880 cotton expressed sequence tags (ESTs; CC ACN45220-ACN63099). The ESTs were isolated from cDNA libraries generated CC variety Coker 312 Boswell 96 Field, and androecium tissue, gynoecium CC vissue, developing fibres, carpel walls and septa from variety coker 312 Boswell 96 Field, and androecium tissue, gynoecium CC variety Coker 312 Boswell 96 Field, and androecium tissue, gynoecium CC invention3B. The invention also relates to substantially purified CC proteins or their fragments encoded by nucleic acid molecules of the CC invention, and to transformed plants having a nucleic acid construct comprising a nucleic acid of the invention. The cotton ESTs are useful as CC molecular tags to isolate genetic regions, to isolate genes, to metabolic cariety of agronomically significant genes are useful for isolating a variety of agronomically significant genes are classiciated with plant growth, quality, yield, and could also serve as clinks in metabolic and catabolic pathways. The nucleic acid molecules may be useful for identifying genes important in initiating and maintaining call germination or that may be used to mitigate stresses encountered conductors and cis-regulatory elements which will be useful to express conductally significant genes in these tissues and/or other tissues, genetic and molecular mapping, and in cloning of agronomically conductant genes. The nucleic acid molecules are further useful for detecting the expression level or pattern of a protein or manA and for CC detecting the presence or quantity of a protein by tissue printing. The
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ZIEGLER T
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16-MAR-2000;
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                                                                                               isolated nucleic acid mol
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                         Page 11585; 11750pp; English
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                                                                         presence of prostate cancer,
                                                                      nucleic acid molecule associated with cancerous state and correlating with presence of prostate cancer, use presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer; cytostatic; carcinogen;
marker; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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Best Local Similarity
Matches 134; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cotton; plant; EST; expressed sequence tag; transgenic plant; seed; variety DP50B; library LIB3825; molecular tag; molecular marker; genetic mapping; molecular mapping; seed germination; plant growth; plant quality; plant yield; plant breeding; tissue printing; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cancer has metastatized in a patient; (f) assessing the aggressiveness or indolence of prostate cancer in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                         (FENG/)
                                                                                                                                                                                                                                                                               12-DEC-2001;
                                                                                                                                                                                                                                                                                                                                 24-JUN-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Gossypium hirsutum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cotton primed seed EST Clone ID: LIB3825-005-Q1-N6-D10,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 626 BP; 356 A; 15 C; 41 G; 130 T; 0 U;
  WPI; 2004-479808/45
                                                    Deikman
                                                                                                                                                                                                                             14-DEC-2000; 2000US-0255619P
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FENG P C C.
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                                                                                                 FINCHER K L.
ZIEGLER T E.
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ilarity 48.0%;
Conservative
                                               Feng PCC,
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                                                  Fincher KL,
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0; Mismatches
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Pred. No. 0.11;
                                                  Ziegler TE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 5;
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CC from primed or non-primed seeds from variety DPSOB, mature seeds from CC variety Coker 312 Boswell 96 Field, and androecium tissue, gynoecium CC variety Coker 312 Boswell 96 Field, and androecium tissue, gynoecium CC Nucotton33B. The invention also relates to substantially purified CC Nucotton33B. The invention also relates to substantially purified CC proteins or their fragments encoded by nucleic acid molecules of the CC comprising a nucleic acid of the invention. The cotton ESTs are useful as molecular tags to isolate genetic regions, to isolate genes, to map CC genes, to determine gene function and to determining whether genes are useful for isolating a variety of agronomically significant genes are CC also useful for identifying genes important in initiating and maintaining seed germination or that may be used to mitigate stresses encountered during seed germination. The ESTs additionally enable the acquisition of promoters and cis-regulatory elements which will be useful to express gronomically significant genes in these tissues and/or other tissues, capronomically significant genes in these tissues and/or other tissues, cc agronomically significant genes in these tissues and/or other tissues, cc and also permits the acquisition of molecular markers useful in breeding schemes, genetic and molecular mapping, and in cloning of agronomically contents the expression level or pattern of a protein or maNA and for detecting the expression level or pattern of a protein or maNA and for cotton variety DPSOB primed seed cnNA library (LIB3825). The sequence cotton variety DPSOB primed seed cnNA library (LIB3825). The sequence cotton variety DPSOB primed seed cnNA library (LIB3825). The sequence cotton variety DPSOB primed seed cnNA library (LIB3825). The sequence cotton variety DPSOB primed seed cnNA library (LIB3825). The sequence cotton variety DPSOB primed seed cnNA library (LIB3825). RESULT 11
ABZ10100
ID ABZ10 5 В Ş 맑 Ş 밁 S 밁 Ş ZXXX Matches 144; Query Match 8.5%; Best Local Similarity 50.7%; New isolated nucleic acid molecule that encodes a plant protein or its fragment, useful for isolating a variety of agronomically significant genes associated with plant growth, quality or yield, and as molecular tags to ACN45220-ACN63099). The Sequence 499 BP; 212 A; 32 C; 62 G; 193 T; 0 U; 0 Other; seqdata.uspto.gov/sequence.html?DocID=US20040123340 16-JAN-2003 ABZ10100 ABZ10100 standard; DNA; 8056 BP 1; SEQ ID NO 1716; 34pp; English 154 425 305 94 34 map genes. TAGTACTTGTTTTTCTTTTTGGGTTCAACTAGTTACTTTTTTCCTTTGACATCAAAATT GGCTTGGCAAGATTCCATAAGTTTATTTCACCAAAAAGGAAAGA attgtagacgagtggtccatatatagatggtgaaatgaaatgaatattgagtaataaata <u>АДДАДДАДДАДДАДДАДДАДДАДДАДДАДДАДДАДАДДАДДАДДАДДАДДАДДАДДАДДАДДАД</u> TGTAAFTAAGTTTTATGAAATGTGGTTATTTTGTAGGTCACGTGAAATTTATTAATTTT Conservative (first entry) to 17880 cotton expressed sequence tags (ESTs; ne ESTs were isolated from cDNA libraries generated 0; Score 60; DB 1 Pred. No. 0.11; 0; Mismatches 0.11; DB 13; Length 499; 140; Indels 588

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Gaps

484 153 424 93

273 544 213

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differentiating between haematopoietic cell proliferative disorders considered with at least 1 gene and/or their regulatory regions in a considered with at least 1 gene and/or their regulatory regions in a considered with at least 1 gene and/or their regulatory regions in a considered with at least 1 gene and/or their regulatory regions in a considered with at least 1 reagent, considered distinguishes between methylated and non-methylated CPG which distinguishes between methylated and non-methylated CPG dinucleotides within the target nucleic acid. ABZ09861 to ABZ1118 converted invention. Oligonucleotides from the present from the present for convention of ligonucleotides from the present invention can be used: for convention the cytosine methylation for cells and proliferative disorder haematopoietic cells; for differentiating between acute convention to leukaemia; as probes for convention to leukaemia; as probes for convention of haematopoietic cell proliferation disorder related sequences and their complements; and as primers for the convention of haematopoietic cell proliferation disorder related DNA sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between convention cell proliferative disorders. The present method enables a highly specific cels proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders and informed treatment of patients. S 밁 8 밁 S Query Match Best Local S Matches 272 Human; haematopoietic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia; cytosine methylation state; gene; ds. Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent the distinguishes between methylated and non-methylated CpG dinucleotides. Olek A, 03-OCT-2002 Homo sapiens. Haematopoietic cell proliferation disorder related DNA sequence #240 Claim 28; WPI; 2003-018942/01. Berlin (EPIG-) EPIGENOMICS 26-MAR-2001; 2001US-0278333P 26-MAR-2002; 2002WO-EP003401. WO200277272-A2 Sequence Lewin A, disorders allowing for improved and informed treatment present invention describes a method for detecting and 2109 11 l Similarity 272; Conserv ~ Piepenbrock C, Adorja Lipscher E, Maier S, ATTTGGGAAAATTTAATAATATATGTATTAAATGGCAAATAAAAGTTAGATGAGAGTTTT 8056 BP; TTTAAATTTTTATTATAAAAAATTATTTTTTGCATGAAATTGTTTTTAAGATAAAATTTTG ACATAACCAAGTATTATTTTCCGCCACGAATTGAGTCTACGAGAGATGTCCTGTCTTTAA 190 SEQ ID NO 240; 117pp; English. Braun A, Conservative 3711 A; 371 C; 371 G; 3603 T; 0 U; 0 Other; 8.4%; Distler J, tler J, Guetig D, Adorjan P, Grabs aier S, Model F, 0; Score 59.4; DB 8; Pred. No. 0.16; 0; Mismatches 336; Howe A,
G, Lesche R,
Gar V, Otto T 8; Length 8056; Indels Mueller J; 1; ш Gaps

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RESULT 12
ABK31495
ID ABK31
XX
ABK31495
AC ABK31
XX
DT 23-AI
XX
CDG
KW Huma
KW Huma
KW CDG
KW anti
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PN WO2
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PD 03-
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PD 03-
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PR 30.
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PR 30.
PR 30.
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                                                                                                                                        Oligonucleotide for diagnosis and therapy of diseases associated with signal transduction e.g. cancer, comprises chemically modified genomic sequences of genes associated with signal transduction.
                                                                                 Claim 1; SEQ ID NO 338; 24pp; English
                                                                                                                                                                                                                                                                                                            Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                          30-JUN-2000; 2000DE-01032529.
01-SEP-2000; 2000DE-01043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; signal transduction associated gene; cytosine methylation state; CpG island; signal transduction associated disease; solid tumour; cancer; antitumour; cytostatic; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal transduction associated gene modified complementary DNA #169
                                                                                                                                                                                                                                                          WPI; 2002-147896/19
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The present invention relates to chemically modified DNA sequences of signal transduction associated genes. The DNA sequences are chemically

30-JUN-2000; 2000DE-01032529 01-SEP-2000; 2000DE-01043826

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cc modified using a solution of bisulphite, hydrogen sulphite or disulphite. Also disclosed are oligonucleotides and/or PNA oligomers for detecting ct he cytosine methylation state (CpG islands) of these genes, and a method cf or the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with signal transduction. The genomic DNA can be cobtained from cells or cellular components which contain DNA, e.g. cell clines, biopaies, blood, sputum, stool, urine, cerebral-spinal fluid, ctissue embedded in paraffin such as tissue from eyes, intestine, kidney, cc tissue embedded in paraffin such as tissue from eyes, intestine, kidney, cc tissue embedded in paraffin such as tissue from eyes, intestine, kidney, cc transuction, beart, prostate, lung, breast or liver, histologic object slides, and all their possible combinations. The sequences of the invention are useful for the diagnosis and therapy of diseases associated with signal transduction, or their complements before the sequence of the printed combination, but was obtained in electronic format directly from the sequences. Note: The sequences are considered with signal transduction, or their complementary sequences. Note: The sequence data for this patent did not form part of the printed sequences for the printed complements. The printed sequences are considered with signal transduction, or their complements of the printed sequences.
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Best Local
                                                                             29-JUN-2001; 2001WO-EP007471
                                                                                                                                                         WO200202807-A2
                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                                   Cell signalling; cytosine methylation; cell signalling disease; cancer; tumour; cytostatic; ds.
                                                                                                                                                                                                                                                                                           Chemically treated cell signalling DNA sequence complementary to#179.
                                                                                                                                                                                                                                                                                                                                      01-JUL-2002
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Pred. No. 0.16;
0; Mismatches 151;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                     ADQ24856 standard;
                                                                                                                                      Human soft tissue sarcoma-upregulated DNA - SEQ ID 7676.
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                                                                        sarcoma;
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                                                                                                                                                                                                                                                                                                                                                         DNA; 6816
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                                                                        gene therapy; vaccine; screening;
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Best Local S
Matches 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6816 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; SEQ ID NO 7676; 210pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-NOV-2002; 2002US-0429739P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           specification per se but was submitted in CD format by the inventor.
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                                                                                                                                                                                                                                                                                                                                       AGTTTTTTAAATTTTTTATAAAATAATTTTTTGCATGAAATTGTTTTTAAGATAAA 124
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                                                                                            TGTAATTAAGTTTTATGAAATGTGGTTATTTTGTAGGTCACGTGAAATTTATTAATTTTT
                                                                                                                                 AAANAAAANTNAAAATATTTTTTTTTTTTTTTTT----TTNCCNNAAAAAATAATAATAA 6419
                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTTAAATTTTGGGAAAATTTAATAATATATGTATTAAATGCCAAATAAAAGTTAGATGAG
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                                                                                                                                                                   TACCGGTTAATAATATTCTAACCGGTTTATAAGTTTACATAAATCATTTACTAATCCGCG 304
                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>,,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 59.2; DB 12; Length Pred. No. 0.17; o; Mismatches 222; Indels
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DT O1-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Comprising a polynucleotide encoding a protein operably linked with a CC heterologous promoter sequence. The invention also concerns methods for CC providing gene therapy for genetic deficiency disorders. Vectors of the CC invention are useful for delivering a polynucleotide encoding a protein CC particle, or by transfection, transduction, or injection either in vitro CC or in vivo. The vector is useful for the vertebrate cell by infection in a viral CC particle, or by transfection, transduction, or injection either in vitro CC or in vivo. The vector is useful for the delivery and expression of CC biologically useful proteins in gene therapy protocols, and for CC delivering large DNA segments for engineering of vertebrate cells.

CC Polynucleotides of the invention have applications in techniques such as their use as insertion sites for foreign genes of interest, hybridisation CC production of sense or antisense nucleic acids. Vectors of the invention probes, for chromosome and gene mapping, in PCR technologies, and in the production of stable integration and expression of heterologous DNA in host cells, and are adapted for accepting large heterologous DNA in host cells, and are adapted for accepting large heterologous DNA in host called the control of the genus be delivered in an infected or transformed cell and ceragement of the genome of the genus B entomopoxvirus from amsacta moorei (AmEPV)
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Best Local Similarity 54.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 50000 BP; 20514 A; 4505 C; 4614 G; 20367 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 150-175; 326pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-AUG-2000; 2000US-0224479P.
14-SEP-2000; 2000US-00662254.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a recombinant entomopox virus (EPV) vector,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              promoter sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-AUG-2001; 2001WO-US025287
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TTTTTTGGGTTCAACTAGTTACTTTTTTCCTTTGACAAAAATTATTGTAGACGAGTGG 439
                                                               TAATATTTTTTÄATTTCTÄTTATAAGATATTTTTTATTATATTTTGCTATGTTATTATT
                                                                                                                                     TGAAATGTGGTTATTTTGTAGGTCACGTGAAATTTATTAATTTTTTAGTACTTGTTTTTC 379
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Search completed: November 17, 2005, 15:59:37
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AL069706 Drosophil
AL069440 Drosophil
AL167941 Tetraddon
AL063921 Drosophil
AL099163 Drosophil
AL106578 Drosophil
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CR667281 Tetraodon AL206908 Tetraodon			AL099642 Drosophi	CF547155 AGENCOURT	CG749728 P044-1-C0	CV480279 AGENCOURT	CK156432 FGAS03740	CF519392 AGENCOURT	AL106121 Drosophil	AZ549422 ENTDP49TF	AL229763 Tetraodon	AL063921 Drosophi	AL106396 Drosophi	AL067978 Drosophi	AG396050 Mus muscu	AG386981 Mus muscu	AL103735 Drosophi	AL103554 Drosophi	CL078758 CH216-15

## ALIGNMENTS

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ACCESSION
VERSION
KEYWORDS
SOURCE
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AUTHORS
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165;
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster genome survey sequence SP6 end of BAC BACNISCIS of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
AL106171
AL106171.1 GI:5620504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genoscope.
Direct Submission
                                                                                                          Similarity
                                                                                                                                                                                         /organism="Drosophila melanogaster"
/mol_type="genomic_DNA"
/db_xref="taxon.7227"
/clone="BACN15C18"
/clone_ib="DrosBAC"
/plasmid="pBeloBAC11"
/note="end : SP6"
                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                          10.6%;
                                                                                  Score 75; DB 9
Pred. No. 0.001
29; Mismatches
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survey sequence SP6 end of BAC
                                                                                                        DB 9; Length 1225; 0.0013;
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RESULT 2
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Geoegawa and Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw ap, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fl
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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                                                   Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
Direct Submission
Submitted (02-JUN-1999)
BP 191 91006 EVRY cedex
                                                                                                                                Ely), genomic survey sequence.
ALO69440
ALO69440 GI:4949583
GSS.
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BACR29P01 of RPCI-98 library from
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                                     Genoscope
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/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR29B23"
/clone_lib="RPCI-98"
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Genoscope - Centre - FRANCE (E-mail :
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                                                                 WWKGGKGKKKTKGGGGGKGTGGGGDARAARAAKGKGTTKGTKGTKGKTARTTTKTTTK 1097
                                                                                                                                                                     AACAAAAAAAATTAGTGGAAAAGGTAACTGGAAAGAAAAGGCTTATTGGCTTGGCAAGAT 557
                                                                                                                                                                                                                                                                           WATTTTTTTAWWTAAWAWTGTAATWAAATTAWWTTAAAAAWAATGWTTTWTAAATTWWGT 918
                                                                                                                                                                                                                                                                                                         TCTTTTTTGGGTTCAACTAGTTACTTTTTCCTTTGACATCAAAATTATTGTAGACGAGT 437
                                                                                                                                                                                                                                                                                                                                             TATTCTAACCGGTTTATAAGTTTACATAAATCATTTACTAATCCGCGTGTAATTAAGTTT 317
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Location/Qualifiers
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/note="end : TET3"
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/db_xref="taxon:7227"
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ALI67541.1 GI:7805598
ALI67541.1 GI:7805598
GSS; genome survey sequence.
Getraodon nigroviridis
Tetraodon nigroviridis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Roest Crollius, H., Jaillon, O., Dasilva, C., Bernot, A., Fizames, C., Wincker, P., Brottien Saurin, W. and Weissenbach, J.

    - Web : www.genoscope.cns.fr)
    This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tecraodon nigroviridis
genome. For more information, please take a look at

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196C24 of library G from Tetra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tetraodon nigroviridis
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                                                                                                                                                     ATTTTGACATAACCAAGTATTATTTTCCGCCACGAATTGAGTCTACGAGAGATGTCCTGT
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PUC-Ori"
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/mol_type="genomic DNA"
/db_xref="teaxon:99883"
/clone="196C24"
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Pred. No. 0.0041;
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACGAC Resource Center can be found at http://barnac.med.buffalo.
                                                                                                                                                                                 1100
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ALOGRAPI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                                                                       WWWWWATWDTWWDKWWWWATAAKTDTAWTWWRTAWRADWAGRDRGAGKRDRDAATDADGA
                                          TCCGCCACGAATTGAGTCTACGAGAGATGTCCTGTCTTAAACCTCGTAAAGTTTTGGTC
                                                                                                                                                                                 KARRWGDDTWDRDTRKDDWDWTKWWTWWKDRADDRRWAGDADRWAWDDGAGTWWTATWWW 1041
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/db_xref="taxon:7227"
/clone="back08K10"
/clone_lib="RPCI-98"
/note="end: TET3"
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                                                                                                                                                                                                                                                                        10.3%; Score 72.4; DB 9
18.5%; Pred. No. 0.0039;
tive 283; Mismatches 26
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                                                                                                                                                       Direct Submission

Direct Submission

Direct Submission

Submitted (23-UIL-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC

library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNS010MP 734 bp DNA linear GSS 26-JUL-19
Drosophila melanogaster genome survey sequence T7 end of BAC
DROSOPHILA melanogaster (fruit
DACN04120 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (fruit fly)
Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 734)
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                                     /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
                       /clone="BACN04L20"
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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY Cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of
                                                                                   Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1200)
                                                                                                                                                                                                                          CNS016CO 1200 bp DNA linear GSS 26-JUL-1: Drosophila melanogaster genome survey sequence T7 end of BAC BACN15E04 of DrosbAC library from Drosophila melanogaster (fruit
                                                                                                                                                                       AL106578.1
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Pred. No. 0.0077;
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                                                                                                                                                                     CR722884
Tetraodon nigroviridis full-length cDNA.
CR722884.1 GI:51221135
HTC; CDNA; full-length; Tetraodon nigroviridis.
Tetraodon nigroviridis
Tetraodon nigroviridis
Tetraodon nigroviridis
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoide; Tetraodontidae; Tetraodon.
Direct Submission
Submitted (10-AUG-2004) Genoscope - Centre National de Submitted (10-AUG-2004) Genoscope - Centre Natio
                                                                                                                   Genoscope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pBeloBAC11.
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/plasmid="pBeloBAC11"
/note="end : T7"
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/db_xref="taxon:7227"
/clone="BACN15E04"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
More information available at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ഗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.genoscope.cns.fr/tetraodon.
                                                                                                               CNS00DKY 928 bp DNA linear GSS 04-JUN-1999 Drosophila melanogaster genome survey sequence T7 end of BAC # BACR27A24 of RPCI-98 library from Drosophila melanogaster (fruit
        Drosophila melanogaster
Eukaryota; Metazoa; Archropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 928)
                                                             Drosophila melanogaster (fruit fly)
                                                                                   AL071865.1
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                                                                                                        genomic survey sequence.
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/db_xref="taxon:99883"
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                                                                                    GI:4948170
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Direct Submission

Submitted (02-UN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oscegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
                                                                                                                                                                                                                                                                           CNS0021J 1101 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR05N11 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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AL061936.1 GI:4940214
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/mol type="genomic DNA"
/db xref="taxon:7227"
/clone="BACR27A24"
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/note="end : T7"
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Determination of this BAC-end sequence was carried out as
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/clone_lib="RPCI-98"
/note="end : T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
1 (bases 1 to 886)
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BH177277
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Contact: Pierce RJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: Raymond.Pierce@pasteur-lille.fr
CNS sequencing ID=DGOAA008DF11BP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Institut Pasteur de Lille
1 rue du Professeur A. Calmette, 59019-Lille, France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Class: BAC ends
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Fax: (33) (0)3 20877888
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                                                            AGTTTTTTAAATTTTTTATAAAATAATTTTTTGCATGAAATTGTTTTAAGATAAA 124
                                                                                                                       TTTTAAATTTGGGAAAATTTAATATATATATGTATTAAATGGCAAATAAAAGTTAGATGAG
  ATTTTGACATAACCAAGTATTATTTTCCGCCACGAATTGAGTCTACGAGAGATGTCCTGT 184
                                       AWITTYTYTTWTTWTTTAATIWTATAAAWTTANATTATTAWTTTTTTTTTAAAATTTTT
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                                                                                                                                                                                                                                                                                                                      /lab_host="Biomphalaria glabrata"
/clone lib="SmBAC1"
/clone lib="SmBAC1"
/clone lib="SmBAC1"
/note="Vector: pBeloBAC 11; Site_1: Hind III; Partially
/note="Vector: pBeloBAC 11; Site_1: Hind III digested and size-selected S. mansoni cercarial
bua was ligated into Hind III digested pBeloBAC 11 vector
and used to transform E. coli pBH10B. The complete library
contains 23808 clones from 4 independent
size sizing-ligation-transformations. Average insert size
                                                                                                                                                                                                                                                                                                 sizing-ligation-transformations. Average insert size ranges from 70-127 kb and genome coverage is 7.9-fold."
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/strain="Puerto-Rican"
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T3 end of clone 008DF11 of library SmBAC1 from strain Puerto-Rican
of Schistosoma mansoni, genomic survey sequence
AL614235
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                                                                                                                                                                                                           Web: www.genoscope.cns.fr)

Partially Hind III digested and size-selected S. mansoni cercarial DNA was ligated into Hind III digested pBeloBAC 11 vector and used to transform E. coli DHIOB. The complete library contains 23808 clones from 4 independent sizing-ligation-transformations. Average insert size ranges from 70-127 kb and genome coverage is 7.9-fold.
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BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
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                                                                       /db_xref="taxon:6183"
/clone="008DF11"
                                                                                                                             /organism="Schistosoma mansoni"
/mol_type="genomic DNA"
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                               /clone_lib="SmBAC1"
/note="end : T3"
                                                                                                               /strain="Puerto-Rican"
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Best Local Similarity
Matches 198; Conserv
                                                                                                            ALZ52144.1 GI:7973166
ALZ52154.1 GI:7973166
GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Torradontoidea; Tetraodontidae; Tetraodon.
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                                                             Estimate of human gene number provided by using Tetraodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)
                                                                                                   Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C. Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F.,
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1 (bases 1 to 1592)
Srinivasan,J., Sinz,W., Jesse,T.,
Buntjer,J., van der Meulen,M. and
                                                                                                                                                                                                 Pristionchus pacificus
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Pristionchus pacificus
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/db_xref="taxon:99883"
/clone="040G05"
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FEATURES
Search completed: November 17, 2005, 17:46:28 Job time : 3124 secs
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/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Ppa EcoRI BAC Library"
/clone_lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest of the genomic DNA with EcoRI and cloning into the BAC vector."
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Match Length
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1: /cgn2_6/ptcdatta/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptcdatta/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptcdata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptcdata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptcdata/1/ina/PCTUS_COMB.seq:*
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Gapop 10.0 , Gapext 1.0
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Peterson, David S. Su, Xin-zhaun Wellems, Thomas E.

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TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEPAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
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SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/487,826B FILING DATE: 10-SEP-1993 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: AN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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TYPE: nucleic acid
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T: 620 Newport Center Drive 16th Floor
Newport Beach
: California
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Pred. No. 0.13;
0; Mismatches 244;
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US-09-949-016-12776/c
Sequence 12776, Application US/09949016
Sequence 12776, Application US/09949016
Sequence 12776, Application US/09949016
Parent NO. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12776
LENGTH: 187169
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Best Local
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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LOCATION: (1)...(187169)
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                                                             TTTTAGTACTTGTTTTTCTTTTTGGGTTCAACTAGTTACTTTTTTCCTTTGACATCAAA
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig
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Best Local Similarity
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CURRENUT NONT FOR THE POLYMORPHY NONT FOR THE PROPERTY NONT FOR THE PROPERTY NONT FOR THE POLYMORPHY NONT FOR THE POLYMORPHY
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LOCATION: (1)...(191569)
OTHER INFORMATION: n = A,T,C
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Conservative
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RESULT 5 US-09-790-988-1/c ; Sequence 1, Application US/09790988 ; Patent No. 6632935 ; GENERAL INFORMATION:

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GENERAL INFORMATION:
APPLICANT: The University of British Columbia
TITLE OF INVENTION: Regulation of Embryonic Tran
FILE REFERENCE: 4810-58741
CURRENT APPLICATION NUMBER: US/09/806,708B
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/147,133
PRIOR APPLICATION NUMBER: US 60/147,133
PRIOR FILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.0
SEQ ID NO 22
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US-09-806-708B-22/c
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SEQ ID NO 1
LENGTH: 640681
                                                                                                                                                                                                                                                                    Sequence 22, Application US/09806708B Patent No. 6784342
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Best Local Similarity 47.2%;
Matches 225; Conservative
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CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: JP2000-107160
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
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APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF
FILE REFERENCE: 081356/0159
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APPLICANT: WATANABE, HIDEMI
APPLICANT: HATTORI, MASAHIR
                   LENGTH: 1141
TYPE: DNA
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ORGANISM: Artificial sequence
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Pred. No. 0.34;
0; Mismatches 244;
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; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1141)
; OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. FAE1 promoters
US-09-806-708B-22
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 207012
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Best Local S
Matches 74
                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                    Sequence 15270, Application US/09949016
Patent No. 6812339
                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1):..(192302)
; OTHER INFORMATION: n = A
US-09-949-016-15270
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SEQ ID NO 15270
LENGTH: 192302
                                                                                                                                                                                                                                                                                                       GENERAL INFORM
APPLICANT:
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Best Local Similarity
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,410
                                                                                                                                                                                                                   APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                     ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
                                                                                                                     COUNTRY: U
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Knechtle, Philipp
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Steiner, Sabine
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US/08/998,416

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Sequence 22, Application US/09806708B
Sequence 22, Application US/09806708B
Patent No. 6784342
GENERAL INFORMATION:
APPLICANT: The University of British Columbia
TITLE OF INVENTION: Regulation of Embryonic Transcription
FILE REFERENCE: 4810-58741
CURRENT APPLICATION NUMBER: US/09/806,708B
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMUDICATION INFORMATION:
TELEPHONE: 919-541-8587
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Pred. No. 0.2;
0; Mismatches 274;
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PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 1999-08-04;
NUMBER OF SEQ ID NOS: 23;
SOFTWARE: PATENTIN VERSION 3.0;
SEQ ID NO 22;
LENGTH: 1141
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Sequence 17061, Application US/09949016
PATENT NO. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTEN, J. CRAIG et al.
APPLIC
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Best Local !
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ORGANISM: Artificial sequence
FEATURE:
NAME/KEY: promoter
LOCATION: (1) . (1141)
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12.5%; Pred. No. 0
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PRIOR APPLICATION NUMBER: 00/23/,00

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version

SEQ ID NO 124813
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; ORGANISM: Human
US-09-949-016-124813
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 17061
LENGTH: 96922
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Best Local
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
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PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                      APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
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ORGANISM: Human
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44.9%;
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Pred. No. 0.45;
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OF DETECTION AND USES THEREOF
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US-09-573-080A-29
                                                US-09-573-080A-29
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Best Local
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APPLICANT: JOAN, KNOLL
APPLICANT: ROGAN, PETER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 29, Application US/09573080A Patent No. 6828097
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 29
Query Match
Best Local Similarity
                                                                                                                                                                              NAME/KEY: repeat region
LOCATION: (1)...(696)
OTHER INFORMATION: hervg25
OTHER INFORMATION: n is a, c, g or t
PUBLICATION INFORMATION:
PUBLICATION INFORMATION:
AUTHORS: Jurka, J; Malichiewicz, J; Milosavljevic, A
TITLE: Prototypic sequences for human repetitive DNA
JOURNAL: Journal of Molecular Evolution
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/573,080A CURRENT FILING DATE: 2000-05-16
                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                JOURNAL: Jo
VOLUME: 35
                                                              DATABASE ACCESSION NUMBER: Database DATABASE ENTRY DATE: DATABASE ENTRY DATE: 1996-01-26
                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                PAGES: 286-291
DATE: 1992-10-
                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                  ISSUE:
                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 6996
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milarity 47.6%;
Conservative
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 Score
Pred.
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No. 0.
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-0-31
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
ISEQ ID NO 28913
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                                                                                                     ; ORGANISM: Human US-09-949-016-28913
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US-09-949-016-28913/c
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
FILE REFERENCE: CL001307
                                 Query Match 6.9%;
Best Local Similarity 49.6%;
Matches 122; Conservative
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 277 GTTTACATAAATCATTTACTAATCCGCGTGTAATTAAGTTTTATGAAATGTGGTTATTTT 336
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                                                    Score 48.8; DB 4;
Pred. No. 0.29;
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                                  Mismatches
                                    123;
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RESULT 15
US-09-270-767-29671/c
; Sequence 29671, Application US/09270767
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; ORGANISM: Human US-09-949-016-125860
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US-09-949-016-125860/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 207012
SOPTWARE: FastSEQ for Windows Version
SEQ ID NO 125860
LENGTH: 601
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
CURRENT FILING DATE: 2000-04-14
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Best Local Similarity
Matches 122; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                                                                         GTTACTTTTTTCCTTTGACATCAAAATTATTGTAGACGAGTGGTCCATATATAGATGGTG
                                                                                                                                                                                                                                                                                  TTGKATATTATATATATTGTAAATTATATTACAATATATTCTATATTGTAATATATTG
                                                                                                                                                                                                                                                                                                                          GTAGGTCACGTGAAATTTATTAATTTTTTAGTACTTGTTTTTTCTTTTTTGGGTTCAACTA 396
                                                                                                                                                                                                                                                                                                                                                                                                                       GTTTACATAAATCATTTACTAATCCGCGTGTAATTAAGTTTTATGAAATGTGGTTATTTT
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                                          AAAGGT 522
                                                                                                                                     AAATGAAATGAATATTGAGTAATAAATAAATATAGAAAGTGAACAAAAAAATTAGTGGA
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AATGGT 119
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Pred. No. 0.29;
1; Mismatches 123;
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; Patent No. 6703491
; GENERAL INFORMATION:
APPLICANT: HOMBUIGER et al.
; APPLICANT: HOMBUIGER et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 29671
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-29671
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Search completed: November 17, 2005, 17:49:32 Job time : 179 secs
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Best Local Similarity 52.2%;
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                201 GTTTTGGTCTTACCCAACCCAAT 223
                                                                                                                                                                                 141 GTATTATTTTCCGCCACGAATTGAGTCTACGAGAGATGTCCTGTCTTTAAACCTCGTAAA 200
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                                                                                                                                                                                                                                                     81 TTATTATAAATTATTTTTGCATGAAATTGTTTTTAAGATAAAATTTTGACATAACCAA 140
                                                                                                                                               83 CTTTTGATTATAATGCCACTGCGCACTTGAATAAGCTGAGCCAACTTATTAACTTTAACA 24
                                                                         23
                                                                       CTTTCGTAATGAACCAACACAAT 1
                                                                                                                                                                                                                                                                                                                                                                         Score 47.8; DB 4; Length 927; Pred. No. 0.5; O; Mismatches 97; Indels
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Minimum
Maximum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Run on:
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DB seq length: 2000000000
                                           November 17, 2005, 15:51:38 ; Search time 850 Seconds (without alignments) 6859.085 Million cell updates/sec
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705
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Published_Applications_NA:*
| Cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
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| Cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US10B_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US0B_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US0B_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US0B_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US0B_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

O 43247	Result No.
705 704 64.2 62.6	Score
100.0 99.9 9.1 8.9 8.9	Query
705 2017 8056 8056 531	ength
201221	BB
21 US-10-810-788A-4 21 US-10-810-788A-3 21 US-10-473-126-386 21 US-10-473-126-386 21 US-10-021-323-6375	ID
Sequence 4, Appli Sequence 3, Appli Sequence 386, App Sequence 386, App Sequence 6375, Ap	Description

6.4 8.0 553 21 US-10-425-115 6.2 8.0 17848 15 US-10-239-676 6.2 8.0 17848 16 US-10-240-453 6.2 8.0 17848 18 US-10-257-166 5.6 7.9 517 20 US-10-021-323 56 7.9 560 20 US-10-021-323	.1 577 1 .1 8423 1 .0 376 1 .0 574 2 .0 385 1
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553 21 US-10-425-115-3994 7848 15 US-10-239-676-28 7848 16 US-10-240-453-38 7848 18 US-10-257-166-58 517 20 US-10-021-323-1105 560 20 US-10-021-323-2253	577 1 423 1 376 1 574 2 385 1 385 1
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	-10-424-599-1359 -10-311-455-1380 -09-814-353-1858 -10-021-323-1114 -09-814-353-5368
Sequence 28, Sequence 28, Sequence 38, Sequence 58, Sequence 11055 Sequence 2253	ល ល ល ល ល

## ALIGNMENTS

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US-10-810-788A-4
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                                                                                                                                                                            SUFILL
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/10810788A Publication No. US20040216184A1 GENERAL INFORMATION:
                                                                  Matches
                                                                                   Best
                                                                                                 Query Match
                                                                                                                                                                                                           APPLICANT: Ruezinsky, Diane
TITLE OF INVENTION: Novel Plant Promoters for Use in Early Seed Development
FILE REFERENCE: REN-00-118
CURRENT APPLICATION NUMBER: US/10/810,788A
CURRENT FILING DATE: 2004-03-26
FRIOR APPLICATION NUMBER: US 60/458,828
PRIOR PRIOR PILING DATE: 2003-03-28
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.1
                                                                                                                                          TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                    Local 705;
                                                                                Similarity
100.0%; Score 705; DB 21; llarity 100.0%; Pred. No. 3.2e-122; Conservative 0; Mismatches 0;
                                                                                               Length 705;
                                                                0
                                                                Gaps
   60
                                                                0
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Sequence 3, Application US/10810788A

Publication No. US20040216184A1

GENERAL INFORMATION:
APPLICANT: Ruezinsky, Diane
TITLE OF INVENTION: Novel plant promoters for Use in FILE REFERICE: REN-00-118

CURRENT APPLICATION NUMBER: US/10/810,788A

CURRENT FILING DATE: 2004-03-26

PRIOR APPLICATION NUMBER: US 60/458,828

PRIOR APPLICATION NUMBER: US 60/458,828

PRIOR APPLICATION NUMBER: US 50/458,828

INUMBER OF SEQ ID NOS: 17

SOFTWARE: PatentIn version 3.1

SEQ ID NO 3

LENGTH: 2017

TYPE: DNA ORGANISM: Arabidopsis thaliana

US-10-810-788A-3
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                                                         Query Match
Best Local Similarity
Matches 704; Conserv
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                  AAGCTTTTAAATTTGGGAAAATTTAATATATATATGTATTAAATGGCAAATAAAAGTTAGA
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                                                        99.9%; Score 704; DB 21; Length 2017; ilarity 100.0%; Pred. No. 7.1e-122; Conservative 0; Mismatches 0; Indels 0
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5 TITTAAATTTGGGAAAATTTAATAATATATATATATAAATGGCAAATAAAAGTTAGATGAG 64 	/ Match 9.1%; Score 64.2; DB 21; Length 8056; Local Similarity 45.7%; Pred. No. 0.059; Les 260; Conservative 0; Mismatches 308; Indels 1; Gaps 1;	WESULT 3  US-10-473-126-386/c  US-10-473-126-386, Application US/10473126  Publication No. US20040234973A1  GENERAL INFORMATION:  APPLICANT: Epigenomics AG  TITLE OF INVENTION: methods and nucleic acids for the analysis of hematopoietic cell  TITLE OF INVENTION: proliferative disorders  FILE REFERENCE:  CURRENT APPLICATION NUMBER: US/10/473,126  CURRENT FILING DATE: 2003-09-26  NUMBER OF SEQ ID NOS: 1258  SEQ ID NO 386  LENGTH: 8056  TYPE: DNA  ORGANISM: Artificial Sequence  FEATURE:  COTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  US-10-473-126-386	661 TCAAAACATATTTGGCGTTATTATTTCTGTGGTCACTTGAATAC 704	GCTCTCTCTCTTTTAAAATGGTAAACTGGTAAAGATAGGAGACTCAATTTCTAGTTCA	1854 TATTGGCTTGGCAAGATTCCATAAGTTTATTTCACCAAAAAGGAAAGATACTTGGCCTT 1913	541 TATTGGCTTGGCAAGATTCCATAAGTTTATTTCACCAAAAAGGAAAGATACTTGGCCTT 600	481 AATAAATATAGAAAGTGAACAAAAAAATTAGTGGAAAAGGTAACTGGAAAGAAA	421 AATTATTGTAGACGAGTGGTCCATATATAGATGGTGAAATGAAATGAATATTGAGTAATA 480                1734 AATTATTGTAGACGAGTGGTCCATATATAGATGGTGAAATGAAATGAATATTGAGTAATA 1793	361 TTTTAGTACTTGTTTTTCTTTTTTGGGTTCAACTAGTTACTTTTTTCCTTTGACATCAA 420	301 CGCGTGTAATTAAGTTTATGAAATGTGGTTATTTTGTAGGTCACGTGAAATTTATTAAT 360 	241 ACCATACCGGTTAATAATATTCTAACCGGTTTATAAGTTTACATAAATCATTTACTAATC 300 	181 CTGTCTTTAAACCTCGTAAAGTTTTGGTCTTACCCAACCCAATACCCACAAAGGTAAACG 240	121 TAAAATTTTGACATAACCAAGTATTATTTTCCGGCACGAATTGAGTCTACGAGAGAGA	61 TGAGAGTTTTTTTAAATTTTTTATTATAAATAATTTTTTT

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Matches
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TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
TITLE OF INVENTION: proliferative disorders
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/473,126
CURRENT FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 1258
SEQ ID NO 386
LENGTH: 8056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 386, Applic Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                        OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                 Local Similarity 45.0%; Score 62.6; DB 21; Local Similarity 45.0%; Pred. No. 0.12; hes 274; Conservative 0; Mismatches
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                              ACATAACCAAGTATTATTTTCCGCCACGAATTGAGTCTACGAGAGATGTCCTGTCTTTAA 190
                                                               TTTAAATTTTTTATTATAAAATAATTTTTTGCATGAAATTGTTTTTAAGATAAAATTTTG 130
                                                                                                                             AAATTAATAAAAATAATAATTTTTTTT
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o. US20040234973A1
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US-10-021-323-6375
US-10-021-323-6375, Application US/10021323
; Publication No. US20040123340A1
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GENERAL INFORMATION:

APPLICANT: Deikman, Jill

APPLICANT: Fincher, Karen L.

APPLICANT: Fincher, Karen L.

APPLICANT: Ziegler, Todd E.

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(52274)B

CURRENT APPLICATION NUMBER: US/10/021,323

CURRENT FILING DATE: 2001-12-12

PRIOR APPLICATION NUMBER: US 60/255, 619

PRIOR APPLICATION NUMBER: US 60/255, 619

PRIOR TILING DATE: 2000-12-14

NUMBER OF SEQ ID NOS: 17880

SEQ ID NO 6375

LENGTH: 531
                                                                                                                             Matches 144;
                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                       NAME/KEY: unsure
LOCATION: (1)..(531)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: LIB3828-004-Q1-N6-H2
                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Gossypium
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TTTTCTTTTTTGGGTTCAACTAGTTACTTTTTTCCTTTGACATCAAAATTATTGTAGACG
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Pred. No. 0.051;
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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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APPLICANT: Epigenomics AG
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic
TITLE OF INVENTION: proliferative disorders
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/473,126
CURRENT APPLICATION NUMBER: US/10/473,126
CURRENT FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 1258
SEQ ID NO 240
LENGTH: 8056
TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 248; Conserv
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Publication No. US20040234973A1
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                      ATTGTAGACGAGTGGTCCATATATAGATGGTGAAATGAAATGAATATTGAGTAATAAATA 484
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46.1%;
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US-10-311-455-191
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, OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-311-455-191
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Publication No. US20030143606A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determi
TITLE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
CURRENT FILING DATE: 2002-12-16
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SEQ ID NO 191
LENGTH: 11422
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Best Local Similarity
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PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
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                                        GCTTGGCAAGATTCCATAAGTTTATTT 572
                                                                                                                     ATATAGAAAGTGAACAAAAAAATTAGTGGAAAAGGTAACTGGAAAAGAAAAGGCTTATTG 545
                                                                                                                                                                                                                                                                          TTTAGAATTATGTGAGATAGTATTTAATTGTATTAGAATTT---ATTAAAAGAAAAACGA
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                                                                                        AGTACTTGTTTTTCTTTTTGGGTTCAACTAGTTACTTTTTTCCTTTGACATCAAAATTA 425
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7762
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US-10-257-166-17
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US-10-257-166-17
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Best Local S
Matches 272
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Publication No. US20040023230A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Method and Nucleic Acids for Analysing the Methylation
TITLE OF INVENTION: Genes Implicated in Pharmacogenomics
FILE REFERENCE: 5013.1011
CURRENT APPLICATION NUMBER: US/10/257,166
CURRENT FILING DATE: 2002-10-07
CURRENT FILING DATE: 2002-10-07
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NUMBER OF SEQ ID
SEQ ID NO 17
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ORGANISM: Artificial Sequence
FEATURE:
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DE 10043826.1
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TATAGATTTAATATTTTATTTTATTT
                          GCTTGGCAAGATTCCATAAGTTTATTT 572
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                                                        Conservative
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Pred. No. 0.31;
0; Mismatches 284;
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Sequence 60960, Application US/10357930

Publication No. US20040259086A1

GENERAL INFORMATION:

APPLICANT: Schlagel Robert

APPLICANT: Endege, Wilson

APPLICANT: Monahan, John

ITITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, ITITLE OF INVENTION: HUMAN PROSTATE CANCER

FILE REFERENCE: MRI-007BCN

CURRENT FILING DATE: 2003-02-04

PRIOR APPLICATION NUMBER: 09/785,276

PRIOR APPLICATION NUMBER: 60/183,319

PRIOR FILING DATE: 2000-03-16

PRIOR APPLICATION NUMBER: 60/183,319

PRIOR APPLICATION NUMBER: 60/183,319
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US-10-021-323-2253/c
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APPLICANT: Fincher, Karen L.
APPLICANT: Ziegler, Todd E.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(52774)
CURRENT APPLICATION UNMBER: US/10/021,323
CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION UNMBER: US 60/255, 619
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 17880
SEQ ID NO 2253
LENGTH: 560
TYPE: DNA
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Publication No. US/20040123340A1
GENERAL INFORMATION:
APPLICANT: Deikman, Jill
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Best Local Similarity
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ilarity 50.7%;
Conservative
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Pred. No. 0.
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; OTHER INFORMATION: n = A, T, C
US-10-357-930-60960
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US-10-021-323-1716
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SEQ ID NO 60960
LENGTH: 626
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          NUMBER OF SEQ ID NOS: 17880
SEQ ID NO 1716
LENGTH: 499
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Best Local Similarity
Matches 134; Conserv
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LOCATION: 447, 451, 453, 4
LOCATION: 515, 529, 538, 5
LOCATION: 581, 582, 584, 5
LOCATION: 618
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PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR PILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
                                                     APPLICANT: Fincher, Karen L.
APPLICANT: Ziegler, Todd E.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (52274)B
CURRENT APPLICATION NUMBER: US/10/021,323
CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 60/255, 619
PRIOR PILING DATE: 2000-12-14
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LOCATION: 48, 49, 50, 117, 135, 136, 137, 166, 168, 189, 194, 197,
LOCATION: 227, 251, 253, 277, 278, 279, 281, 291, 323, 324, 327, 328,
LOCATION: 329, 331, 336, 337, 338, 339, 371, 372, 376, 377, 379, 381,
LOCATION: 382, 394, 403, 404, 405, 406, 408, 413, 429, 431, 437
OTHER INFORMATION: n = A,T,C or G
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ORGANISM: Homo sapiens
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TYPE: DNA
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Pred. No. 0.14;
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, OTHER INFORMATION: Clone ID: LIB3825-005-Q1-N6-D10
US-10-021-323-1716
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US-10-473-126-240
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                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/473,126
CURRENT FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 1258
SEQ ID NO 240
SEQ ID NO 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 240, Application US/10473126
Publication No. US20040234973A1
GENERAL INFORMATION:
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Methods and nucleic acids for the analysis of
TITLE OF INVENTION: proliferative disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 8056
TYPE: DNA
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                                                                                                                                                                                       TTTAAATTTTTTATTATAAAATAATTTTTTGCATGAAATTGTTTTTAAGATAAATTTTG 130
                                                                                                                                                                                                                      GGCTTGGCAAGATTCCATAAGTTTATTTCACCAAAAAGGAAAGA 588
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                                                                               АССТССТАВАВСТТТТССТТАСССВАСССВАТАСССВСВАВАВСТАВАССВССВТАСССС
                                                                                                            ACATAACCAAGTATTATTTTCCGCCACGAATTGAGTCTACGAGAGATGTCCTGTCTTTAA 190
TTAATAATATTCTAACCGGTTTATAAGTTTACATAAATCATTTACTAATCCGCGTGTAAT 310
                                                                                                                                                                                                                                                                           8.4%; ilarity 44.7%; Conservative
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; Pred. No. 0.46
0; Mismatches
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Pred. No. 0.14;
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RESULT 13
US-10-723-860-7676/c
Sequence 7676, Application US/10723860
Publication No. US20040253606A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Zlotnik, Albert
               OTHER INFORMATION: n is FEATURE:
                                                                        NAME/KEY: misc feature
LOCATION: (6215)..(6221)
OTHER INFORMATION: n is a,
                                                                                                                         NAME/KEY: misc feature LOCATION: (6209)..(6209) OTHER INFORMATION: n is
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LOCATION: (3223)..(3247)
OTHER INFORMATION: n is a,
                                                                                                                                                                                                                                                                              NAME/KEY: misc feature LOCATION: (1919)..(1989) OTHER INFORMATION: n is
                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
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LOCATION: (6189)..(6189)
OTHER INFORMATION: n is
                                      NAME/KEY: misc feature
NAME/KEY: misc_feature
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FEATURE:
NAME/KEY:
LOCATION:
            FEATURE:
NAME/KEY:
                              FEATURE: misc feature LOCATION: (6388)..(6388) OTHER INFORMATION: n is
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LOCATION: (6341)..(6342)
OTHER INFORMATION: n is
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NAME/KEY: misc_feature
LOCATION: (6324)..(6327)
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LOCATION: (6322)..(6322)
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LOCATION: (6307)...(6307)
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LOCATION: (6248)..(6248)
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LOCATION: (6276)..(6276)
OTHER INFORMATION: n is
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NAME/KEY: misc_feature
LOCATION: (6250)..(6250)
OTHER INFORMATION: n is
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LOCATION: (6261)..(626
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OTHER INFORMATION: n is
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NAME/KEY: misc feature LOCATION: (6470)...(6470) OTHER INFORMATION: n is
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LOCATION: (6465)..(6465)
OTHER INFORMATION: n is
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LOCATION: (6463)..(6463)
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LOCATION: (6434)..(6435)
OTHER INFORMATION: n is
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LOCATION: (6483)..(6483)
OTHER INFORMATION: n is
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OTHER INFORMATION: n is
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LOCATION: (6416)..(641
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OTHER INFORMATION: n is
                                             NAME/KEY: misc_feature
LOCATION: (6642)..(6642)
OTHER INFORMATION: n is
                                                                                NAME/KEY: misc feature LOCATION: (6619)..(6620) OTHER INFORMATION: n is FEATURE:
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LOCATION: (6607)..(6607)
OTHER INFORMATION: n is
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LOCATION: (6562)..(6563)
OTHER INFORMATION: n is
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NAME/KEY: misc feature
LOCATION: (6557)..(6557)
OTHER INFORMATION: n is
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LOCATION: (6534)..(6536)
OTHER INFORMATION: n is
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LOCATION: (6517)..(6517)
OTHER INFORMATION: n is a,
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OTHER INFORMATION: n is
NAME/KEY: misc_feature
LOCATION: (6644)..(6646)
OTHER INFORMATION: n is
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LOCATION: (6494)..(649
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LOCATION: (6485)..(648
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US-10-706-635-24
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                                                         ; ORGANISM: Amsacta
US-10-706-635-24
                                                                                                                                                          CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: 09/086,651
PRIOR FILING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: 09/662,254
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/224,479
PRIOR FILING DATE: 2000-08-10
                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       Sequence 24, Application US/10706635
Publication No. US20050014263A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 186;
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Best Local Similarity
Query Match
Best Local Similarity
Matches 138; Conserv
                                                                                                     SEQ ID NO 24
LENGTH: 50000
                                                                                                                                                                                                                                                     APPLICANT: L1, Y1
TITLE OF INVENTION: Materials and Methods
TITLE OF INVENTION: Verrebrate Cells
FILE REFERENCE: UF-221C1XCZ1
CURRENT APPLICATION NUMBER: US/10/706,635
CURRENT FILING DATE: 2003-11-12
                                                                                                                                                                                                                                                                                                                               APPLICANT: Moyer, Richard W. APPLICANT: Li, Yi
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                                                                                                                                                 NUMBER OF SEQ ID NOS: 80
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NAME/KEY: misc_feature
LOCATION: (6660)..(6660)
OTHER INFORMATION: n is
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OTHER INFORMATION: n is
                                                                                         TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 ATTTTGACATAACCAAGTATTATTTTCCGCCACGAATTGAGTCTACGAGAGATGTCCTGT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245
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Pred. No. 0.48;
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Pred. No. 0.94;
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                                DB 22;
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Search completed: November 17, 2005, 18:03:54 Job time : 855 secs
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US-10-021-323-16830
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CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 60/255, 619
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 17880
SEQ ID NO 16830
LENGTH: 469
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 8.4%; Score 59; DB 20; Length 469; Best Local Similarity 51.3%; Pred. No. 0.21; Matches 137; Conservative 0; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 16830, Application US/10021323 Publication No. US20040123340A1 GENERAL INFORMATION:
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APPLICANT: Feng, Paul C.C.
APPLICANT: Fincher, Karen L.
APPLICANT: Ziegler, Todd E.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(52274)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Gossypium hirsutum
FEATURE:
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                                                                       251
                                                                                                                                         330 TTATTTTGTAGGTCACGTGAAATTTATTAATTTTTTAGTACTTGTTTTTTCTTTTTTGGGT 389
                                                                                                                                                                                                                                                                                                                                                                                    270 TTTATAAGTTTACATAAATCATTTACTAATCCGCGTGTAATTAAGTTTTATGAAATGTGG 329
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                                                                     TTTAAAAAAAAAAAAAAAAAAAAA 277
                                                                                                       TAGTGGAAAAGGTAACTGGAAAGAAAA 536
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